OM nucleic - nucleic search, using sw model

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Run on: April 6, 2005, 12:28:42 ; Search time 5374.67 Seconds
                                             (without alignments)
                                    10403.867 Million cell updates/sec

Title: US-09-904-584-2
Perfect score: 1154
Sequence: 1 atggactcccgatccagat.........ccagtatgactagtcgtgga 1154

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	Str	ID	Description
1	1152.4	99.9	1154	9		HSU17298	U17298 Human kappa
2	1152.4	99.9	1179	6		CQ723157	CQ723157 Sequence
3	1152.4	99.9	1604	9		HUMOPRK1B	L37362 Homo sapien
4	1144.4	99.2	1182	6		AR270854	AR270854 Sequence
5	1144.4	99.2	1182	6		AX548862	AX548862 Sequence
6	1144.4	99.2	1182	6		AX774764	AX774764 Sequence
7	1144.4	99.2	1182	9		HSU11053	U11053 Human kappa
8	1141.4	98.9	1143	6		AR281679	AR281679 Sequence
9	1140.4	98.8	1142	6		A48343	A48343 Sequence 1
10	1140.4	98.8	1142	6		AR141371	AR141371 Sequence
11	1138.2	98.6	1143	9		AF498922	AF498922 Homo sapi
12	1136.2	98.5	1284	6		AR281680	AR281680 Sequence
13	1130.2	97.9	1143	6		AX280919	AX280919 Sequence
14	1056.8	91.6	1396	9		AY168006	AY168006 Homo sapi
15	999.4	86.6	1275	6		AR281681	AR281681 Sequence
16	994.6	86.2	1275	6		AR281682	AR281682 Sequence
17	933.8	80.9	1733	10		CPU04092	U04092 Cavia porce
18	912.4	79.1	1273	10		RATRORD	D16534 Rattus norv
19	912.4	79.1	1358	10		RATKOR1A	L22001 Rat kappa o
20	910.8	78.9	4742	10		RNU00442	U00442 Rattus norv
21	909.2	78.8	1288	10		S81111	S81111 kappa-opioi
22	909.2	78.8	1408	6		A68828	A68828 Sequence 5
23	909.2	78.8	1408	6		AR409589	AR409589 Sequence
24	909.2	78.8	1410	6		AR105149	AR105149 Sequence
25	909.2	78.8	1410	6		AR178399	AR178399 Sequence
26	909.2	78.8	1410	10		MUSKAPOPRE	L11065 Mouse kappa
27	909.2	78.8	2094	10		RATKOR1B	L22536 Rattus norv
28	909.2	78.8	2481	6		E08874	E08874 cDNA coding
29	909.2	78.8	2481	10		RATKOR	D16829 Rattus norv
30	869.6	75.4	1000	6		AR105156	AR105156 Sequence
31	869.6	75.4	1000	6		AR178406	AR178406 Sequence
32	632.2	54.8	757	4		PIGKOR	L49437 Sus scrofa
33	590.2	51.0	715	4		AF012105	AF012105 Sus scrof
34	577	50.0	1941	5		AY725197	AY725197 Taricha g
35	544.4	47.2	179356	2	c	AC083844	AC083844 Homo sapi
36	544.4	47.2	183519	9	c	AC009646	AC009646 Homo sapi
37	512.2	44.4	1454	5		AF530573	AF530573 Rana pipi
38	489.8	42.4	1477	5		AF285173	AF285173 Danio rer
39	469.2	40.7	562	11		BV209418	BV209418 OPRK1_334
40	453.6	39.3	1120	5		AY728087	AY728087 Taricha g
41	449.4	38.9	1387	5		AF132813	AF132813 Danio rer
42	446.4	38.7	2135	6		AR148257	AR148257 Sequence
43	446.4	38.7	2135	10		RATMUOR1A	L20684 Rattus norv
44	446.4	38.7	2397	10		RATRORB	D16349 Rattus norv
45	444.8	38.5	1401	10		RATMOPIOID	L22455 Rat mu opio

ALIGNMENTS

RESULT 1
HSU17298

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LOCUS       HSU17298                1154 bp    mRNA    linear   PRI 14-JUL-1995
DEFINITION  Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION   U17298
VERSION     U17298.1  GI:596069
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1154)
  AUTHORS   Simonin,F., Gaveriaux-Ruff,C., Befort,K., Matthes,H., Lannes,B.,
            Micheletti,G., Mattei,M.G., Charron,G., Bloch,B. and Kieffer,B.
  TITLE     kappa-Opioid receptor in humans: cDNA and genomic cloning,
            chromosomal assignment, functional expression, pharmacology, and
            expression pattern in the central nervous system
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)
  MEDLINE   95350200
   PUBMED   7624359
REFERENCE   2  (bases 1 to 1154)
  AUTHORS   Manson,E., Bare,L. and Yang,D.
  TITLE     Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL   Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE   94338360
   PUBMED   8060324
REFERENCE   3  (bases 1 to 1154)
  AUTHORS   Kieffer,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Superieure De
            Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Illkirch,
            67400, France
FEATURES             Location/Qualifiers
     source          1..1154
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="8"
                     /map="8q11-12"
                     /tissue_type="placenta"
     gene            1..1154
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CDS             1..1143
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                /note="G-protein coupled; transmembrane protein"
                /codon_start=1
                /product="kappa opioid receptor"
                /protein_id="AAC50158.1"
                /db_xref="GI:596070"
                /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
                EDAQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLA
                LADALVTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAV
                CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMIRLKSVRLLSGSREKDRNLRRITRLV
                LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"

ORIGIN

Query Match     99.9%;      Score 1152.4; DB 9; Length 1154;
Best Local Similarity     99.9%;      Pred. No. 1.2e-201;
Matches 1153;   Conservative    0;   Mismatches    1;   Indels    1;   Gaps    0;

Qy    1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCCGAGCGCC    60
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Db    1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCCGAGCGCC    60

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   120
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Db   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   120

Qy  121 AGCGGCCGCTCGGAGGACGCGCCAGCTGGAGCCCGGCCGCCCGCCACATCTCCCCGGCCATCCCGGTC  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGCGGCCGCTCGGAGGACGCGCCAGCTGGAGCCCGGCCGCCCGCCACATCTCCCCGGCCATCCCGGTC  180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCGAACTCGCTGGTC  240
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Db  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCGAACTCGCTGGTC  240

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
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Db  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTCGTGCAAGATAGTAATTCCATTGATTACTAC  420
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Db  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTCGTGCAAGATAGTAATTCCATTGATTACTAC  420

Qy  421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC  540
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Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC  540

Qy  541 TGCATCTGGCTGCTGTCGTCCTCATCGTTGGCATCGTTGGCAATAGTCCTTGAAGGCACCAAA  600
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Db  541 TGCATCTGGCTGCTGTCGTCCTCATCGTTGGCATCGTTGGCAATAGTCCTTGAAGGCACCAAA  600

Qy  601 GTCAGGGAAGACGTGCGATGTCATTGAGTGTCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Db  601 GTCAGGGAAGACGTGCGATGTCATTGAGTGTCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy  661 TGTTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC  720
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Db  661 TGTTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC  720

Qy  721 ATCATCATCGTCTGCTACCCCGTCACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
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Db  721 ATCATCATCGTCTGCTACCCCGTCACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGGTGGTGGTG  840
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Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGGTGGTGGTG  840
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Qy  841 GCAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCACTATTCATCCTCGGTGGAGGCTCTCGGGG  900
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Db  841 GCAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCACTATTCATCCTCGGTGGAGGCTCTCGGGG  900

Qy  901 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCATCGCCTTAGGCTAT  960
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Db  901 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCATCGCCTTAGGCTAT  960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020
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Db  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAATGGAGCGGCAGAGCACTAGCAGAGTC  1080
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Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
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Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy 1141 TGACTAGTCGTGGA  1154
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Db 1141 TGACTAGTCGTGGA  1154
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RESULT 2
CQ723157

LOCUS       CQ723157               1179 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 9091 from Patent WO02068579.
ACCESSION   CQ723157
VERSION     CQ723157.1   GI:42284014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 9091 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1..1179
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match     99.9%;      Score 1152.4;  DB 6;  Length 1179;
Best Local Similarity     99.9%;      Pred. No. 1.2e-201;
Matches 1153;   Conservative    0;   Mismatches    1;   Indels    1;   Gaps    0;

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Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   120
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Db   71 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   130

Qy  121 AGCGGCCGCTCGGAGGACGCGGAGCCGAGTCGGAGCCCACATCTCCCGGCCATCCCGGTC  180
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Db  131 AGCGGCCGCTCGGAGGACGCGGAGCCGAGTCGGAGCCCACATCTCCCGGCCATCCCGGTC  190

Qy  181 ATCATCACGGCGCGTCTACTCCGTAGTGTTCGTGTGGGCGCAACTCGCTGGTC  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  191 ATCATCACGGCGCGTCTACTCCGTAGTGTTCGTGTGGGCAACTCGCTGGTC  250
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SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 1604)
AUTHORS       Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and
              Liu-Chen,L.-Y.
TITLE         Cloning of a human ,kappa opioid receptor from the brain
JOURNAL       Life Sci. 56, 201-207 (1995)
COMMENT       Original source text: Homo sapiens (clone d2-115) (tissue library:
              genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA
              to mRNA.
FEATURES      Location/Qualifiers
     source   1..1604
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              /map="8q11.2"
              /clone="d2-115"
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              /dev_stage="fetus"
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              ZAPII"
     gene     1..1604
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              /codon_start=1
              /product="kappa opioid receptor"
              /protein_id="AAA63906.1"
              /db_xref="GI:722618"
              /db_xref="GDB:G00-132-651"
              /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAWPPGWAEPDSNGSAGS
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              LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
              ENFKRCFRDFCFPLKMRERQSTSRVRNTVQDPAYLRDIDGMNKPV"
ORIGIN
Query Match       99.9%;   Score 1152.4;  DB 9;   Length 1604;
Best Local Similarity   99.9%;    Pred. No. 1.2e-201;
Matches 1153;  Conservative   0;  Mismatches   0;  Indels   1;   Gaps     0;

Qy        1 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGAGGCCCTACCTGCGCCCCCGAGCGCC   60
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Db      378 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGAGGCCCTACCTGCGCCCCCGAGCGCC  437

Qy       61 TGCCTGCCCCCCAACAGCAGCGCCTGGTTCCCGGGCTGGGCCGAGCCCGACAGCAACGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 TGCCTGCCCCCCAACAGCAGCGCCTGGTTCCCGGGCTGGGCCGAGCCCGACAGCAACGGC  497

Qy      121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCCTCCCGGCCATCCCGGTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      498 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCCTCCCGGCCATCCCGGTC  557

Qy      181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGTCTTGTCGTGGGTCTGGTC  240
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Db      558 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGTCTTGTCGTGGGTCTGGTC  617

Qy      241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTACATATTTAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      618 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTACATATTTAAC  677

Qy      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG  360
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Db      678 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG  737

Qy      361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
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Db      738 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  797
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Query Match            99.2%;  Score 1144.4;  DB 6;  Length 1182;
Best Local Similarity  99.5%;  Pred. No. 3.7e-200;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60
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Db     14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 73

Qy     61 TGCCTGCCCCAACAGCAGCGCGCCTGGTTCCCGGCGGGCCGAGCCGCAGCAACGGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 AGGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCGCGACATCTCCCGGGCCATCCCGGTC 180
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Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGCTGCTC 240
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Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACACATTTACATATTTAAC 300
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Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACACATTTACATATTTAAC 313

Qy    301 CTGGCTTTGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGTCTGCAAGATAGTAGTAATTTCATTGATTACTAC 420
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Db    374 ATGAATTCCTGGCCTTTGGGGATGTGTCTGCAAGATAGTAGTAATTTCATTGATTACTAC 433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 480
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Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 493

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCCACCAAA 613

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCCAGATGATGACTACTCC 673

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTCCTC 733

Qy    721 ATCATCATCGTCTGCTCGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCGGTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 ATCATCATCGTCTGCTCGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCGGTTCT 793

Qy    781 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy    841 GCAGTCTTCGTTGTCTGCTGAGACTCCATTCATCCTGGTGGAGGCTCGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 GCGGTTTTCGTCGTCTGCTGAGACTCCATTCATCCTGGTGGAGGCTCGGGG 913

Qy    901 AGCACCTCCCAGCACAGCTGTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AGCACCTCCCACAGCAGCTGTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy    961 ACCAAGTAGCCTGAATCCCATTCTCTTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 ACCAAGTAGCCTGAATCCCATTCTCTTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGCCGGATGGAGCGCAGCGACTAGCAGAGTC 1080
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Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGACCGCTACATTGCCGTG 857

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db    858 TGCCACCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA 917

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA 977

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCCAGATGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCCAGATGATGACTACTCC 1037

Qy    661 TGGTGGGACCCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 TGGTGGGACCCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 1097

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 1157

Qy    781 GGCTCCGAGAGAAAGATCGGCAACCTGCGTAGGATCGGCAACTGGTGCTCTGGTGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 GGCTCCGAGAGAAAGATCGGCAACCTGCGTAGGATCGGCAACTGGTGCTCCGGTGTGGTG 1217

Qy    841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTGGTGAGGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTGGTGAGGGCTCTGGGG 1277

Qy    901 AGCACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 AGCACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1337

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 ACCAACAGTAGCCTGAATCCCATTCTCTTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1397

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGGACGCGGCACTAGCAGAGTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGGACGCGGCACTAGCAGAGTC 1457

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1517

Qy   1141 TGACTAGTCGTGGA 1154
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Db   1518 TGACTAGTCGTGGA 1531
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RESULT 4
AR270854
LOCUS   AR270854   1182 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 1417 from patent US 6500938.
ACCESSION   AR270854
VERSION   AR270854.1 GI:29702088
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1182)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE   Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1417 31-DEC-2002;
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

RESULT 5

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Qy   481  TGCCACCCGTGAAGGCTTGGACTTCCCGCACACCCTTGAAGGCAAAGATCATCAATATC   540
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Db   494  TGCCACCCGTGAAGGCTTGGACTTCCCGCACACCCTTGAAGGCAAAGATCATCAATATC   553

Qy   541  TGCATCTGGCTGCGTGCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554  TGCATCTGGCTGCGTGCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA   613

Qy   601  GTCAGGAGGAAGACGTCGATGTCATTGAGTGCTGTCCCAGATGATGACTGACTACTCC   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614  GTCAGGAGGAAGACGTCGATGTCATTGAGTGCTGTCCCAGATGATGACTGACTACTCC   673

Qy   661  TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCTGTCCTC   720
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Db   674  TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCTGTCCTC   733

Qy   721  ATCATCGTCTGCTACACCCTGATGATCCTGCGTTCAAGAGCGTCCGGCTCCTCTTTCT   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734  ATCATCGTCTGCTACACCCTGATGATCCTGCGTTCAAGAGCGTCCGGCTCCTCTTTCT   793

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGCTGGTCCTGGTGGTGGTG   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGCTGGTCCTGGTGGTGGTG   853

Qy   841  GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGAGGC   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854  GCGGTTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGAGGC   913

Qy   901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCCTTAGGCTAT   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCCTTAGGCTAT   973

Qy   961  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTGATGAAAACTTCAAGCGGTGT   1020
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Db   974  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTGATGAAAACTTCAAGCGGTGT   1033

Qy  1021  TTCCGGGACTTCTGCTTTCCACTGACTGCTTAACCTGAGAAGATGAGGAGCGGCAGAGAGTC   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034  TTCCGGGACTTCTGCTTTCCACTGACTGCTTAACCTGAGAAGATGAGGAGCGGCAGAGAGTC   1093

Qy  1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA   1140
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Db  1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA   1153

Qy  1141  TGACTAGTCGTGGA   1154
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Db  1154  TGACTAGTCGTGGA   1167
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RESULT 5
AX548862
LOCUS       AX548862                 1182 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 147 from Patent WO02061087.
ACCESSION   AX548862
VERSION     AX548862.1  GI:25813740
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 147 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1182
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match             99.2%;  Score 1144.4;  DB 6;  Length 1182;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-200;
  Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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RESULT 6

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Qy     1  ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC    60
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Db    14  ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC    73

Qy    61  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGGCCCAGCAGCAACACGGC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGGCCCAGCAGCAACAACGGC   133

Qy   121  AGCGCCGGCTCCGGAGGACGCGGAGCTGGAGCGCGACGCATCTCCCCGGCCATCCCGGTC   180
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Db   134  AGCGCCGGCTCCGGAGGACGCGGAGCTGGAGCGCGACGCATCTCCCCGGCCATCCCGGTC   193

Qy   181  ATCATCACGGCGGTCACTCCGGTGTCGTAGTGGCTTGTCGTGTGGCAACTCGCTGGTC   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194  ATCATCACGGCGGTCACTCCGGTGTCGTAGTGGCTTGTCGTGTGGCAACTCGCTGGTC   253

Qy   241  ATGTTCGTGATCATCCGATACAACAAGATGAAGACAGCAACCAACATTTACATATTTAAC   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254  ATGTTCGTGATCATCCGATACAACAAGATGAAGACAGCAACCAACATTTACATATTTAAC   313

Qy   301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCTACTCTTG   360
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Db   314  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCTACTCTTG   373

Qy   361  ATGAATTCCTGGCCTTTGGGGATGTCTGTGTCGAAGATAGTAATTCCATTGATTACTAC   420
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Db   374  ATGAATTCCTGGCCTTTGGGGATGTCTGTGTCGAAGATAGTAATTCCATTGATTACTAC   433

Qy   421  AACATGTTCACCAGCATCTTCACCTGACCATGAGCGGTGACCGGCTACATTGCCGTG   480
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Db   434  AACACAGTTCACCAGCATCTTCACCTGACCATGAGCGGTGACCGGCTACATTGCCGTG   493
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RESULT 6
AX774764
LOCUS       AX774764                 1182 bp    DNA     linear   PAT 09-JUL-2003
DEFINITION  Sequence 80 from Patent WO03038129.
ACCESSION   AX774764
VERSION     AX774764.1  GI:32486280
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Raponi,M.
  TITLE     Methods for assessing and treating leukemia
  JOURNAL   Patent: WO 03038129-A 80 08-MAY-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1182
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                     /mol_type="unassigned DNA"
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ORIGIN
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Query Match             99.2%;  Score 1144.4;  DB 6;  Length 1182;
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Db   1034  TTCCGGGACTTCTGCTTCCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1093
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Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGGATGAATAAAACCAGTA 1140
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGGATGAATAAAACCAGTA 1153

Qy   1141  TGACTAGTCGTGGA 1154
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Db   1154  TGACTAGTCGTGGA 1167
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RESULT 7

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HSU11053
LOCUS       HSU11053              1182 bp    mRNA    linear   PRI 22-AUG-1994
DEFINITION  Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION   U11053
VERSION     U11053.1  GI:532059
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1182)
  AUTHORS   Mansson,E., Bare,L. and Yang,D.
  TITLE     Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL   Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE   94338360
   PUBMED   8060324
REFERENCE   2  (bases 1 to 1182)
  AUTHORS   Mansson,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,
            PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA
FEATURES             Location/Qualifiers
     source          1..1182
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="phK1.3"
                     /tissue_type="placenta"
     gene            1..1182
                     /gene="hKOR"
     CDS             14..1156
                     /gene="hKOR"
                     /codon_start=1
                     /product="kappa opioid receptor"
                     /protein_id="AAA20985.1"
                     /db_xref="GI:532060"
                     /translation="MESPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
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                     CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                     LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                     ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"

ORIGIN
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Query Match 99.2%; Score 1144.4; DB 9; Length 1182;
Best Local Similarity 99.5%; Pred. No. 3.7e-200;
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGGCCGGCCCTACCTGCGCCCGAGCGCC 60
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Db     14  ATGGAATCCCGATTCAGATCTTCCGCGGGGAGGCCGGCCCTACCTGCGCCCGAGCGCC 73

Qy     61  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 133

Qy    121  AGGCCGGCCGGCTCGGAGGACAGCGCCAGCTGAGCGTGCCACATCTCCCGGCCATCCCGGTC 180
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134  AGGCCGGCCGGCTCGGAGGACAGCGCCAGCTGAGCGTGCCACATCTCCCGGCCATCCCGGTC 193

Qy    181  ATCATCACGGCGGGGTCTACTCCGTAGTGTTCGTCGTCGGGCTGGTGGGCAACTCGCTGGTC 240
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194  ATCATCACGGCGGGGTCTACTCCGTAGTGTTCGTCGTCGGGCTGGTGGGCAACTCGCTGGTC 253

Qy    241  ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254  ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy    301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTCACTTG 360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTCACTTG 373

Qy    361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy    421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
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Db    434  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493

Qy    481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541  TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Db    554  TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy    601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy    661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGATCCCGTCCTC 720
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGATCCCGTCCTC 733

Qy    721  ATCATCATCGTCTGCTACACACCCTGACGATCCGCGTCTCAAGAGCGTCCGGTCCTCCTTCT 780
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Db    734  ATCATCATCGTCTGCTACACACCCTGACGATCCGCGTCTCAAGAGCGTCCGGTCCTCCTTCT 793

Qy    781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGTCTGGTGGTGGTG 840
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGTCTGGTGGTGGTG 853

Qy    841  GCAGTTCGTCGTTTCGTCGTCTGCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG 900
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Db    854  GCGGTTTTCGTCGTTTCGTCGTCTGCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG 913

Qy    901  AGCACCTCCCACAGCACGGCAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914  AGCACCTCCCACAGCACGGCAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy    961  ACCAACAGTAGCCTGAATCCCATTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974  ACCAACAGTAGCCTGAATCCCATTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021  TTCCGGGACTTCTGCTTCCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
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ACCESSION   AR281679
VERSION   AR281679.1   GI:29717434
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1143)
  AUTHORS   ConKlin,B.R.
  TITLE   Selective target cell activation by expression of a G
             protein-coupled receptor activated superiorly by synthetic ligand
  JOURNAL   Patent: US 6518480-A 1 11-FEB-2003;
FEATURES   Location/Qualifiers
  source   1..1143
                  /organism="unknown"
                  /mol_type="genomic DNA"

ORIGIN

Query Match   98.9%; Score 1141.4; DB 6; Length 1143;
Best Local Similarity   99.9%; Pred. No. 1.3e-199;
Matches 1142; Mismatches 0; Conservative 0; Indels 1; Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60
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Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCAACAGCAGCGGCCTGGTTCCCGGTGGCCGGAGCCCGACAGCAGCAACGGC 120
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Db   61 TGCCTGCCCCAACAGCAGCGGCCTGGTTCCCGGTGGCCGGAGCCCGACAGCAGCAACGGC 120

Qy   121 AGCGGCCGGCTCCGGAGGACGGCAGCTGGAGCGCGGCCGCCATCCGGCTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCCGGCTCCGGAGGACGGCAGCTGGAGCGCGGCCGCCATCCGGCTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACATTACATATTTAAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACATTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGGTGGACCGGTACATTGCCGTG 480
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Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGGTGGACCGGTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCGCACACCCCTGAAGGCAAAGATCATCAATATC 540
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Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCGCACACCCCTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTCGTGTCATCTGTCAATAGTCCTTGGCATCTGCAATCGTTGGACCGTCATTGCCGTG 600
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Db   541 TGCATCTGGCTGCTCGTGTCATCTGTCAATAGTCCTTGGCATCTGCAATCGTTGGACCGTCATTGCCGTG 600

Qy   601 GTCAGGGAAGAGCTGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGAACTACTCC 660
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Db   601 GTCAGGGAAGAGCTGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGAACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGCCTTCGTGATCCTGTCCTC 720
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Db   661 TGGTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGCCTTCGTGATCCTGTCCTC 720

Qy   721 ATCATCATCGTCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780

RESULT 8
AR281679
LOCUS   AR281679   1143 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6518480.

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Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy  841 GCAGTCTTCGTGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
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Db  841 GCAGTCTTCGTGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy  901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Db  901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
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Db  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTC 1080
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Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140

Qy 1141 TGA 1143
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Db 1141 TGA 1143
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RESULT 9
A48343

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LOCUS       A48343        1142 bp    DNA        linear    PAT 07-MAR-1997
DEFINITION  Sequence 1 from Patent WO9601898.
ACCESSION   A48343
VERSION     A48343.1   GI:2302133
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Kieffer,B. and Simonin,F.
  TITLE     HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
  JOURNAL   Patent: WO 9601898-A 1 25-JAN-1996;
            UNIV PASTEUR (FR)
COMMENT     Other publication FR 2722209 960112.
FEATURES             Location/Qualifiers
     source          1..1142
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                     /db_xref="taxon:32644"
     CDS             1..>1142
                     /note="unnamed protein product"
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                     /db_xref="CAA03102.1"
                     /db_xref="GI:2302134"
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                     CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
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                     ENFKRCFRDFCPPLKMRMRQSTSRVRNTVQDPAYLRDIDGMNKPV"
ORIGIN
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Query Match   98.8%;   Score 1140.4; DB 6; Length 1142;
Best Local Similarity 99.9%; Pred. No. 2e-199;
Matches 1141; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Qy   1 ATGGACTCCCCGATCCAGATCTTCCGGGGAGCCCGGGAGCCCTGCCCTGCCCCGAGCGCC 60
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Db   1 ATGGACTCCCCGATCCAGATCTTCCGGGGAGCCCGGGAGCCCTGCCCTGCCCCGAGCGCC 60

Qy  61 TGGCTGCCCCAACAGCAGCCGCGCCTGGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
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Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  61 TGGCTGCCCCAACAGCAGCCGCGCCTGGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120

Db 121 AGGCCGGCTCGGAGGACGCGCAGCTGGAGCCGGCGCACATCTCCCCGGCCATCCCGGTC 180
Qy 121 AGGCCGGCTCGGAGGACGCGCAGCTGGAGCCGGCGCACATCTCCCCGGCCATCCCGGTC 180

Db 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAC 300
Db 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAC 300

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy 361 ATGAATTCCTGGCCTTTGGGGATGTGCTCTGCAAGATAGTAATTTCATTGATTACTAC 420
Db 361 ATGAATTCCTGGCCTTTGGGGATGTGCTCTGCAAGATAGTAATTTCATTGATTACTAC 420

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
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Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTGAAGGCAAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTGAAGGCAAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTCGTCATCTGTTGGCATCTGTTGGCAATAGTCCTTGGAGGACACCAAA 600
Db 541 TGCATCTGGCTGCTCGTCATCTGTTGGCATCTGTTGGCAATAGTCCTTGGAGGACACCAAA 600

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
Db 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
Db 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy 721 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
Db 721 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
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Db 841 GCAGTCTTCGTGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Qy 961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
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Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTC 1080
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140

Qy 1141 TG 1142
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Db      1141 TG 1142

RESULT 10
AR141371
LOCUS       AR141371              1142 bp    DNA        linear    PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6146835.
ACCESSION   AR141371
VERSION     AR141371.1  GI:15100887
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Kieffer,B. and Simonin,F.
  TITLE     Human kappa opioid receptor, nucleic acids and uses thereof
  JOURNAL   Patent: US 6146835-A 1 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1..1142
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ORIGIN

Query Match    98.8%;  Score 1140.4;  DB 6;  Length 1142;
Best Local Similarity  99.9%;  Pred. No. 2e-199;
Matches 1141;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCCGGGGAGCCCGGCCGGGCCCCTACCTGCGCCCGAGCGCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCAGATCTTCCCGGGGAGCCCGGCCGGGCCCCTACCTGCGCCCGAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGGCGGCTGGTTTCCCGGAGCCGAGCCGACAGCAGCAACGGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGGCGGCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAGCAACGGC 120

Qy    121 AGCGCCGCTCGGAGGACGCGGCGAGCTCGGAGCCGCGGCCGCACATCTCCCGGCCATCCCGGTC 180
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Db    121 AGCGCCGCTCGGAGGACGCGGCGAGCTCGGAGCCGCGGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 300
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Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGGCATCTGTTGGACCGGTGGACCGTG 480
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Db    421 AACATGTTCACCAGCATCTTCACCTTGGCATCTGTTGGACCGGTGGACCGTG 480

Qy    481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTGTTGGCAATAGTCCTTGCAGGCACCAAA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTGTTGGCAATAGTCCTTGCAGGCACCAAA 600

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Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGTGATGACTACTCC 660

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTCGTGATCCCTGTCCTC 720
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Db      661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTCGTGATCCCTGTCCTC 720

Qy      721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
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Db      721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy      841 GCAGTCTTCGTTGCTGTCGTGGACTCCATTCACATATTCATCCTGGTGAGGCTCTGGGG 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      901 AGCACCTCCACAGCACAGTCGTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Db      901 AGCACCTCCACAGCACAGTCGTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy      961 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy     1021 TTCCGGGACTTCTGCTTTCACTGAAGATGAGCGGCGGCAGAGCACTAGCAGAGTC 1080
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Db     1021 TTCCGGGACTTCTGCTTTCACTGAAGATGAGCGGCGGCAGAGCACTAGCAGAGTC 1080

Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
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Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy     1141 TG 1142
             ||
Db     1141 TG 1142

RESULT 11
AF498922
LOCUS       AF498922              1143 bp    mRNA       linear    PRI 01-MAY-2002
DEFINITION  Homo sapiens opioid receptor kappa (OPRK1) mRNA, complete cds.
ACCESSION   AF498922
VERSION     AF498922.1  GI:20379019
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1143)
  AUTHORS   Puhl,H.L., Ikeda,S.R. and Aronstam,R.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
            Institute, One Guthrie Square, Sayre, PA 18840, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
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Thu Apr 7 08:55:53 2005

us-09-904-584-2.rge

ORIGIN

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        Query Match      98.6%;   Score 1138.2; DB 9; Length 1143;
        Best Local Similarity  99.7%;   Pred. No. 5e-199;
        Matches 1140;  Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCCCTACCTGCGCCCGAGCGGC 60
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Db     1 ATGGAATCCCGATTCAGATCTTCCGCGGGAGGAGCCCTACCTGCGCCCGAGCGGC 60

Qy    61 TGCCTGCCCCCAACAGCAGCACGCGCCTGGTTTCCCGGCTGGGCCGAGCAACGGC 120
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Db    61 TGCCTGCCCCCAACAGCAGCACGCGCCTGGTTTCCCGGCTGGGCCGAGCAACGGC 120

Qy   121 AGGCGCGGCTCTGGAGGACCGCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGGCGCGGCTCTGGAGGACCGCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGCAACTCGCTCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGCAACTCGCTCGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAGACAGCAACCAACCAACATTTACATATTTAAC 300
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Db   241 ATGTTCGTGATCATCCGATACACAAGACAGCAACCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCACTTG 360

Qy   361 ATGAAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACACATGTTCACCAGCATCTTCACCTTGACCGCTACATTGCCGTG 480
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Db   421 AACACATGTTCACCAGCATCTTCACCTTGACCGCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGACTTCCGCACAATCATCAATATC 540
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Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGACTTCCGCACAATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTCGTGTGTCAATCTCGTGCATCTCTTGGAGGCACCAAA 600
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Db   541 TGCATCTGGCTGCTCGTGTGTCAATCTCGTGCATCTCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACACCTTCTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGTCCTGTCCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACACCTTCTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGTCCTGTCCCTC 720

Qy   721 ATCATCATCGTCTACACCCTGACTAGGATCGCAACCTGCTCAGAGCGTCCCGGCTCCTTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTACACCCTGACTAGGATCGCAACCTGCTCAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAAAGATCGCAACCTGGATCAGCTGGTTCCTGGTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAGAAAGATCGCAACCTGGATCAGCTGGTTCCTGGTGGTGGTG 840

Qy   841 GCAGTTCCTGGCCTTTTGGGATGTGTGCAAGATAGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTTCCTGGCCTTTTGGGATGTGTGCAAGATAGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 900

Qy   901 AGCACCTCCACAGCAGCACGCACAGCTGCTTCTCTCAGCCCTTGACCGCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCAGCACGCACAGCTGCTTCTCTCAGCCCTTGACCGCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCAATCCATTCTTCTTACGCGCCTTTCTTGCGACTTCCGCAACCCTTGAAGGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCAATCCATTCTTCTTACGCGCCTTTCTTGCGACTTCCGCAACCCTTGAAGGGTGT 1020
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Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGACGGCGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGAACTTCTGCTTTCCACTGAAGATGAGACGGCGCAGAGCACTAGCAGAGTC 1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA 1140

Qy  1141 TGA 1143
          |||
Db  1141 TGA 1143
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RESULT 12

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LOCUS          AR281680                    1284 bp    DNA        linear   PAT 10-APR-2003
DEFINITION     Sequence 3 from patent US 6518480.
ACCESSION      AR281680
VERSION        AR281680.1  GI:29717435
KEYWORDS       .
SOURCE         Unknown.
  ORGANISM     Unknown.
               Unclassified.
REFERENCE      1  (bases 1 to 1284)
  AUTHORS      Conklin,B.R.
  TITLE        Selective target cell activation by expression of a G
               protein-coupled receptor activated superiorly by synthetic ligand
  JOURNAL      Patent: US 6518480-A 3 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1..1284
                     /organism="unknown"
                     /mol_type="genomic DNA"
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ORIGIN

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        Query Match      98.5%;   Score 1136.2; DB 6; Length 1284;
        Best Local Similarity  99.7%;   Pred. No. 1.2e-198;
        Matches 1138;  Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy     2 TGGACTCCCCGATCCAGATCTTCCGCGGGAGGAGCCCTACCTGCGCCCGAGCGCCT 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 TCGACTCCCCGATCCAGATCTTCCGCGGGAGGAGCCCTACCTGCGCCCGAGCGCCT 172

Qy    62 GCCTGCCCCCAACAGCAGCAGCGCGCCTGGTTTCCCGGCCGCGAGCCGACGACGGCA 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 GCCTGCCCCCAACAGCAGCAGCGCGCCTGGTTTCCCGGCCGCGAGCCGACGACGGCA 232

Qy   122 GCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCCGGGCCATCCGGTCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 GCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCCGGGCCATCCGGTCA 292

Qy   182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGCAACTCGCTCGGTCA 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGCAACTCGCTCGGTCA 352

Qy   242 TGTTCGTGATCATCCGATACACAAGACAGCAACATGCCTTTCAGAGTACGGTCTCACTTGA 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAGACAGCAACATGCCTTTCAGAGTACGGTCTCACTTGA 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACTACACAACCATGCCTGTGCAAGATAGTAATTTCCATTGATTACTACA 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACTACACAACCATGCCTGTGCAAGATAGTAATTTCCATTGATTACTACA 472

Qy   362 TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 532

Qy   422 ACATGTTCACCAGCATCTTCACCTTGACCGCTACATGAGCGTGCTGT 481
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   533 ACATGTTCACCAGCATCTTCACCTTGACCGCTACATGAGCGTGCTGT 592

Qy   482 GCCACCCCGTGAAGGCTTGACTTCCGCACACCCTTGAAGGGCAAAGATCATCAATATCT 541
          ||||||||||||||||||||||||||||||||||||||||
Db
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Matches 1135;   Conservative 0;   Mismatches 0;   Indels 8;   Gaps 0;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCTACCTGGGCCCGAGCGGCC    60
         |||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGGCCTACCTGGGCCCGAGCGGCC    60

Qy    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCTCGGCCTCGGCCCGACAGCAACGGC   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCTCGGCCTCGGCCCGACAGCAACGGC   120

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCACCCGCGCCATCCCGGTC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCACCCGCGCCATCCCGGTC   180

Qy   181 ATCATCGTCCTGTCTACCTCGGTCTCCAGAGCGTCCGGCAACTCGCTGGTC   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCCTTGGTGGGAACTCGCTGGTC   240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC,  300

Qy   301 CTGGCTTTGGTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA   360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCGTCGAAGAGTAATTTCATTGATTACTAC   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCGTCGAAGAGTAATTTCATTGATTACTAC   420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTGTACATTGCCGTG   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTGTACATTGCCGTG   480

Qy   481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540

Qy   541 TGCATCTGGCTGCTGTCGTCATCGTGTTGGTCATCGTTGCCAGTTCCCAGTTCATTGAGTG   600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCATCGTGTTGGTCATCGTTGCCAGTTCCCAGTTCATTGAGTG   600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAAGATCTGCGGTCTTCGGTCTTCGTCATGAATGACTACTCC   660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAAGATCTGCGGTCTTCGGTCTTCGTCATGAATGACTACTCC   660

Qy   661 TGGTGGGACCTCTTCATGAAGATCGGTACACCGTGCTACCTCCTGCAATCCTGGTCCGGCTCCTTTCT   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCGGTACACCGTGCTACCTCCTGCAATCCTGGTCCGGCTCCTTTCT   720

Qy   721 ATCATCATCGTGCTGCTACACCCTGCGGATCCTGCGATCCTGCGTCTCCAAGAGCGTCCGGCTCCTTTCT   780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTGCTGCTACACCCTGCGGATCCTGCGATCCTGCGTCTCCAAGAGCGTCCGGCTCCTTTCT   780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGCAACTCGCTGGTCCTGGTCTCGGTGGTG   840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGCAACTCGCTGGTCCTGGTCTCGGTGGTG   840

Qy   841 GCAGTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGG   900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGGTGTTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGG   900

Qy   901 AGCACCTCCACAGCACAGCTGTGCTCTCCAGCTATTACTTCTGCATCTCCAGCTATTACTTCTGCATGCCTAT   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCACAGCTGTGCTCTCCAGCTATTACTTCTGCATCTCCAGCTATTACTTCTGCATGCCTAT   960

Qy   961 ACCAACAGTAGCCTGAATCCGATCCCATTCTTCTTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCGATCCCATTCTTCTTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy  1021 TTCCGGGACTTCGCTTTCCACTGAAGATGAGCGGCGGAGTGAGGAGGGCGGCAGCAGTC  1080
         ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCGCTTTCCACTGAAGATGAGCGGCGGAGTGAGGAGGGCGGCAGCAGTC  1080
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Db   593 GCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT   652

Qy   542 GCATCTGGCTGCTGTCGTCATCGTGTTGGTCATCGTTGCCAGTTCCCAGTTCATTGAGTG   601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 GCATCTGGCTGCTGTCGTCATCGTGTTGGTCATCGTTGCCAGTTCCCAGTTCATTGAGTG   712

Qy   602 TCAGGGAAGACGTCGATGTCATTGAAGATCTGCGGTCTTCGGTCTTCGTCATGAATGACTACTCCT   661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   713 TCAGGGAAGACGTCGATGTCATTGAAGATCTGCGGTCTTCGGTCTTCGTCATGAATGACTACTCCT   772

Qy   662 GGTGGGACCTCTTCATGAAGATCGGTACACCGTGCTACCTCCTGCAATCCTGGTCCGGCTCCTTTCTTCTCA   721
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   773 GGTGGGACCTCTTCATGAAGATCGGTACACCGTGCTACCTCCTGCAATCCTGGTCCGGCTCCTTTCTTCTCA   832

Qy   722 TCATCATCGTGCTACACCCTGCGGATCCTGCGTCTCCAAGAGCGTCCGGCTCCTTTCTG   781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   833 TCATCATCGTGCTACACCCTGCGGATCCTGCGTCTCCAAGAGCGTCCGGCTCCTTTCTG   892

Qy   782 GCTCCCGAGAGAAAGATCGCAACCTGCGCAACTCGCTGGTCCTGGTCTCGGTGGTGG   841
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   893 GCTCCCGAGAGAAAGATCGCAACCTGCGCAACTCGCTGGTCCTGGTCTCGGTGGTGG   952

Qy   842 CAGTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA   901
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   953 CAGTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA  1012

Qy   902 GCACCTCCACAGCACAGCTGTGCTCTCCAGCTATTACTTCTGCATCTCCAGCTATTACTTCTGCATGCCTATA   961
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1013 GCACCTCCACAGCACAGCTGTGCTCTCCAGCTATTACTTCTGCATCTCCAGCTATTACTTCTGCATGCCTATA  1072

Qy   962 CCAACAGTAGCCTGAATCCGATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1021
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1073 CCAACAGTAGCCTGAATCCGATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1132

Qy  1022 TCCGGGACTTCGCTTTCCACTGAAGATGAGCGGCGGAGTGAGGAGGGCGGCAGCAGTCC  1081
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1133 TCCGGGACTTCGCTTTCCACTGAAGATGAGCGGCGGAGTGAGGAGGGCGGCAGCAGTCC  1192

Qy  1082 GAAATACAGTCAGGATCTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAT  1141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1193 GAAATACAGTCAGGATCTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAG  1252

Qy  1142 G  1142

Db  1253 G  1253
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RESULT 13

AX280919

LOCUS   AX280919   1143 bp   DNA   linear   PAT 02-NOV-2001

DEFINITION Sequence 542 from Patent WO0177172.

ACCESSION   AX280919

VERSION   AX280919.1 GI:16608215

KEYWORDS   .

SOURCE   Homo sapiens (human)

  ORGANISM Homo sapiens

            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1

  AUTHORS   Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.

  TITLE   Non-endogenous, constitutively activated known g protein-coupled

            receptors

  JOURNAL   Patent: WO 0177172-A 542 18-OCT-2001;

            Arena Pharmaceuticals, Inc. (US)

FEATURES   Location/Qualifiers

  source   1..1143

            /organism="Homo sapiens"

            /mol_type="unassigned DNA"

            /db_xref="taxon:9606"

ORIGIN

Query Match   97.9%; Score 1130.2; DB 6; Length 1143;

Best Local Similarity 99.3%; Pred. No. 1.5e-197;

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140

Qy 1141 TGA 1143
Db. 1141 TGA 1143

RESULT 14
AY168006
LOCUS   AY168006   1396 bp   mRNA   linear   PRI 25-DEC-2002
DEFINITION Homo sapiens DRG kappa 1 splice variant KOR 1A mRNA, complete cds,
            alternatively spliced.
ACCESSION   AY168006
VERSION   AY168006.1 GI:27373027
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1396)
  AUTHORS   Lu,L.D. and Mansson,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371
            Phoenixville Pike, Malvern, PA 19355, USA
FEATURES   Location/Qualifiers
     source   1..1396
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS   237..1337
                     /note="opioid receptor kappa 1A; alternatively spliced"
                     /codon_start=1
                     /product="DRG kappa 1 splice variant KOR 1A"
                     /protein_id="AAN87342.1"
                     /db_xref="GI:27373028"
                     /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAGSEDAQLEPAHISPAI
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                     AKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSIQFPDDDYSWWDLFMKICVFI
                     FAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLVLVVVAVFVVCWTPI
                     HIFILVRALGSTHSHSTAALSSYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPL
                     KMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"
ORIGIN
Query Match   91.6%; Score 1056.8; DB 9; Length 1396;
Best Local Similarity   96.2%; Pred. No. 4.5e-184;
Matches 1110; Conservative   0; Mismatches   2; Indels   42; Gaps   1;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCGGGCCCTACCTGCCCGCCGCC   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 237 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCGGGCCCTACCTGCCCGCCGCC 296

Qy   61 TGCCTGCCCCCCACACAGCAGCGCCTGGTTCCCGGTTCCCCGGCCCGGAGCCCGACAGCAACGGC 120
         |||||||||||||||||||
Db 297 TGCCTGCCCCCCACACA--GC 314

Qy 121 AGCGCCGGCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 315 AGCGCCGGCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 374

Qy 181 ATCATCACGGGGGTCTACTCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 375 ATCATCACGGCGGTCGTCTCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 434

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 435 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 494

Qy 301 CTGGCCTTGGCAGATGCCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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(right column)

Db   495 CTGGCCTTGGCGGAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 554

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
          |||||||||||||||||||||
Db   555 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 614

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||
Db   615 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 674

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCATAATC 540
          |||||||||||||||||||||||||||
Db   675 TGCCACCCGTGAAGGCTTTGGACTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCATAATC 734

Qy   541 TGCATCTGGCTCGTCGTCATCTGTTGGCATCTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||
Db   735 TGCATCTGGCTCGTCGTCATCTGTTGGCATCTGCAATAGTCCTTGGAGGCACCAAA 794

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC 660
          |||||||||||||||||||
Db   795 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC 854

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCTTCGTGATCCCGTCCTC 720
          ||||||||||||||||||||
Db   855 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCTTCGTGATCCCGTCCTC 914

Qy   721 ATCATCGTCTGCTACACACCCGATGATCCTGCGTCTCAAGAGGTCGCGTCCGGCTCCTTTCT 780
          ||||||||||||||||||||
Db   915 ATCATCGTCTGCTACACACCCGATGATCCTGCGTCTCAAGAGGTCGCGTCCGGCTCCTTTCT 974

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGTCTTCGTGGTGGTGGTG 840
          ||||||||||||||||||||
Db   975 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGTCTTCGTGGTGGTGGTG 1034

Qy   841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
          ||||||||||||||||||||
Db 1035 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 1094

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          |||||||||||||||||||
Db 1095 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1154

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||
Db 1155 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1214

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||
Db 1215 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1274

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||
Db 1275 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1334

Qy 1141 TGACTAGTCGTGGA 1154
          |||||||||||
Db 1335 TGACTAGTCGTGGA 1348

RESULT 15
AR281681
LOCUS   AR281681   1275 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6518480.
ACCESSION   AR281681
VERSION   AR281681.1 GI:29717436
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1275)
  AUTHORS   Conklin,B.R.
  TITLE   Selective target cell activation by expression of a G
            protein-coupled receptor activated superiorly by synthetic ligand

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JOURNAL    Patent: US 6518480-A 5 11-FEB-2003;
FEATURES
    source        1..1275
                  /organism="unknown"
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ORIGIN

Query Match      86.6%;  Score 999.4; DB 6;  Length 1275;
Best Local Similarity  93.0%;  Pred. No. 1.6e-173;
Matches 1061;  Conservative  0;  Mismatches 71;  Indels  9;  Gaps  1;

Qy      2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCCCGAGCGCCT 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 TCGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCCT 172

Qy     62 GCCTGCCCCCCAACAGCAGCGGCCGGCCTGGTTCCCGGCTGGGCGCGAGCCGAGACGACAACGGCA 121
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Qy    362 TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421
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Qy    422 ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGT 481
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Qy    902 GCACCTCCCACAGCACAGCAGTCGCTCCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 961
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Db   1004 GCACCTCCCACAGCACAGCAGTCGCTCCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 1063

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Db   1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGAGCGGCGGCAGAGCACTAGCAGAGTCC 1183

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 700.667 Seconds
(without alignments)
9749.831 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 439206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: geneseqm2001as:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1154	100.0	1154	12	ADN30506	Adn30506 Human kap
2	1152.4	99.9	1154	12	ADN30505	Adn30505 Human kap
3	1152.4	99.9	1154	13	ADR44858	Adr44858 Human kap
4	1150.8	99.7	1154	12	ADN30510	Adn30510 Human kap
5	1150.8	99.7	1154	12	ADN30508	Adn30508 Human kap
6	1150.8	99.7	1154	12	ADN30507	Adn30507 Human kap
7	1150.8	99.7	1154	12	ADN30511	Adn30511 Human kap
8	1150.8	99.7	1182	8	AB242678	Abz42678 Human opi
9	1144.4	99.2	1182	10	AAD58490	Aad58490 Human kap
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11	1144.4	99.2	1182	10	ACA56819	Aca56819 Human sig
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13	1144.4	99.2	1182	2	AAT90998	Aat90998 Human kap
14	1141.4	98.9	1143	2	AAT12550	Aat12550 Human kap
15	1140.4	98.8	1142	2	AAT90999	Aat90999 Human kap
16	1136.2	98.5	1284	11	ADL90106	Adl90106 cDNA enco
17	1136.2	98.5	1284	12	ADO30011	Ado30011 Human GPC
18	1133.4	98.2	1143	5	ABI98011	Abi98011 Non-endog
19	1130.2	97.9	1143	2	AAT92601	Aat92601 Human kap
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24	963.4	83.5	1875	11	ADL90118	Adl90118 Human kap
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26	909.2	78.8	1410	2	AAQ75926	Aaq75926 Mouse kap
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28	909.2	78.8	2481	13	AAQ86725	Aaq86725 Mammalian
29	909.2	78.8	2481	13	ADR44862	Adr44862 Rat kappa
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31	877.8	76.1	1911	11	ADL90120	Adl90120 Human kap
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34	444.8	38.5	1401	13	ADR44848	Adr44848 Rat mu-op
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37	444.8	38.3	1618	3	AAS9499	Aas9499 cDNA enco
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40 c	436.8	37.9	9569	13	ADR44842	Adr44842 FIV-NSE-H
41	436.8	37.9	10472	13	ADR44876	Adr44876 Plasmid p
42	434.8	37.7	2162	2	AAV61994	Aav61994 Human mu-
43	434.6	37.7	1464	10	ADG42250	Adg42250 Mu-opioid
44	434.2	37.6	2951	10	ADG42246	Adg42246 Mu-opioid
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ALIGNMENTS

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ID   ADN30506 standard; cDNA; 1154 BP.
XX
AC   ADN30506;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C852T allele.
XX
KW   Human; kappa opioid receptor; hKOR; 88; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity,; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
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PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V,   Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful

```
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 2; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutic effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one additive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C852T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1154;  DB 12;  Length 1154;
Best Local Similarity   100.0%;  Pred. No. 2.7e-274;
Matches 1154;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCTACCTGCCGCCCCGAGCGCC 60
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Qy    61 TGCCTGCCCCCAACAGCAGGCGCCTGGTTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC 120
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Qy   181 ATCATCACGGCGGGGGTCTACTCCGTAGTGTTCGTGGTCGGCCAGCTGGGGCAACTCGCTGGTC 240
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Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
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Qy   481 TGCCACCCCTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
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Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Qy   901 AGCACCTCCACAGCACAGTCTGCTCTCCAGCTATTACTTCTGACATCGGCCTTAGGCTAT 960
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Qy   961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTAGCCTTTCTTGATGAAAACTTCAAGCCGGTGT 1020
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Qy  1141 TGACTAGTCGTGGA 1154
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Db  1141 TGACTAGTCGTGGA 1154
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RESULT 2
ADN30505
ID   ADN30505 standard; cDNA; 1154 BP.
XX
AC   ADN30505;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, wild-type cDNA.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol ; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
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PN   US2004097704-A1.
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PD   20-MAY-2004.
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PF   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Claim 1; SEQ ID NO 1; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to the
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful for
CC   determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the most common, wild-type allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match             99.9%;  Score 1152.4;  DB 12;  Length 1154;
Best Local Similarity   99.9%;  Pred. No. 6.7e-274;
```

```
Matches 1153;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;

Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGGGAGGCGGCCTACCTGCGCCCGAGCGGCGCC     60
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGGGAGGCGGCCTACCTGCGCCCGAGCGGCGCC     60

Qy   61 TGCCTGCCCCCAACACAGCAGCCGCTGGTTCCCGGCTGGCCGAGCCCGGACAGCAGCAACCGC        120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACACAGCAGCCGCTGGTTCCCGGCTGGCCGAGCCCCCACAGCAGCAACCGC        120

Qy  121 AGGGCCGGCTCGGAGGAGACGGCAGCGCAGCTGAGCCCGCACATCTCCCCGGCCATCCGGTC        180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGGGCCGGCTCGGAGGAGACGGCAGCGCAGCTGAGCCCGCACATCTCCCCGGCCATCCCGGTC       180

Qy  181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC        240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC        240

Qy  241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACAACATTTACATATTTAAC        300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACAACATTTACATATTTAAC        300

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTCACTTG      360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTCACTTG      360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC      420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC      420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTG        480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTG        480

Qy  481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC      540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC      540

Qy  541 TGCATCTGGCTGCGTCGTCATCGTTGGTGGCAATAGTCCTTGGAGGCACCAAA        600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCGTCGTCATCGTTGGTGGCAATAGTCCTTGGAGGCACCAAA        600

Qy  601 GTCAGGGAAGACGTGATGTCATTGAGTGCTCCTTGCAGTGCCAGATGACTACTCC        660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTGATGTCATTGAGTGCTCCTTGCAGTGCCAGATGACTACTCC        660

Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC       720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC       720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT       780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT       780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGGTGGTGTG        840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGGTGGTGTG        840

Qy  841 GCAGTCTTCGTTGTCTGCTGGACTCCATTCACATATTCACATATTCTGGTGAGGCTCTGGGG      900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTCTTCGTTGTCTGCTGGACTCCATTCACATATTCACATATTCTGGTGAGGCTCTGGGG      900

Qy  901 AGCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATGCCTTAGGCTAT       960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATGCCTTAGGCTAT       960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT     1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT     1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGCACTAGCAGAGTC      1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGCACTAGCAGAGTC      1080
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Qy      1 ATGGACTCCCGATCCTCAGATCTTCCCGGCGGGAGCCGGGCCCTACCTGCCCGCCCCGAGCGCC 60

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy     61 TGCCTGCCCCCAACAGCAGCGCCGGCCTGTTCCCGGCTCGGCCTCGGCCGGCCGACCAGCAACCGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGCCGGCCTGTTCCCGGCTCGGCCTCGGCCGGCCGACCAGCAACCGC 120

Qy    121 AGCCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG 360

Qy    361 ATGAATTCCTGGCCTTTTGGGATGTGTCTGCAAGATAGTAATTTCCATTGATTACTAC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGATGTGTCTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTCGTCGTCATCGTTGTTGGCATCTCGTCAGTTCCCAGATGACTACTCC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTCGTCGTCATCGTTGTTGGCATCTCGTCAGTTCCCAGATGACTACTCC 600

Qy    601 GTCAGGGAAGACGTCAGGAATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCAGGAATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC 660

Qy    661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy    721 ATCATCATGTCTGCTCACACCCTGCGTCTACACCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATGTCTGCTCACACCCTGCGTCTACACCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACCTGCGTAGGATCACCAGACTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACCTGCGTAGGATCACCAGACTGGTGGTG 840

Qy    841 GCAGTTCTTCGTTGTCGTGCTGACTCCCATTCACATATTCACATATTCATCTCTGCTATTCGTGAGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTTCTTCGTTGTCGTGCTGACTCCCATTCACATATTCACATATTCATCTCTGCTATTCGTGAGGCTCTGGGG 900

Qy    901 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTCTTGATGAAAACTTCAAGCCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTCTTGATGAAAACTTCAAGCCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
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Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154
```

RESULT 3
ADR44858
ID   ADR44858 standard; cDNA; 1154 BP.
XX
AC   ADR44858;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human kappa opioid receptor encoding cDNA SEQ ID NO:30.
XX
KW   opioid receptor; nerve cell; analgesic; gene therapy; pain; human;
KW   kappa opioid receptor; chromosome 8; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1143
FT   /tag= a
FT   /product= "kappa opioid receptor"
XX
PN   WO2004073646-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-US004914.
XX
PR   19-FEB-2003; 2003US-0448663P.
XX
PA   (UYRP) UNIV ROCHESTER.
XX
PI   Kyrkanides S, Tallents RH;
XX
DR   WPI; 2004-635472/61.
DR   P-PSDB; ADR44857.
DR   GENBANK; U17298.
XX
PT   New vector for delivering an opioid receptor to a nerve cell comprising a
PT   sequence encoding a mu-opioid receptor and a vector backbone, useful in
PT   preparing a composition for reducing pain.
XX
PS   Disclosure; SEQ ID NO 30; 147pp; English.
XX
CC   The present invention describes a vector for delivering an opioid
CC   receptor to a nerve cell. The method comprises a sequence encoding an
CC   opioid receptor and a vector backbone. Also described: (1) a cell
CC   comprising the vector or its integrated product; (2) an animal comprising
CC   the cell; (3) reducing pain in a subject; (4) producing the vector; (5)
CC   producing the cell; and (6) an animal produced by the process of
CC   administering the vector to the animal. The vector has analgesic
CC   activity, and can be used in gene therapy. The vector is useful in
CC   preparing a composition for reducing pain in a subject. The present
CC   sequence encodes the human kappa opioid receptor, which is used in the
CC   exemplification of the present invention. The human kappa opioid receptor
CC   gene is located on chromosome 8, more specifically to 8q11-12.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match   99.9%; Score 1152.4; DB 13; Length 1154;
Best Local Similarity 99.9%; Pred. No. 6.7e-274;
Matches 1153; Mismatches 0; Conservative 0; Indels 1; Gaps 0;

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Qy      1 ATGGACTCCCGATCCTCAGATCTTCCCGGCGGGAGCCGGGCCCTACCTGCCCGCCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1141 TGACTAGTCGTGGA 1154
            |||||||||||||
Db     1141 TGACTAGTCGTGGA 1154

RESULT 4
ADN30510
ID   ADN30510 standard; cDNA; 1154 BP.
XX
AC   ADN30510;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, A843G allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   allele         replace(843,A)
FT                  /*tag= a
FT                  /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 6; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system. Also useful for determining neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
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CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is theA843G allele of hKOR.
XX
SQ   Sequence 1154 BP; 238 A; 339 C; 288 G; 289 T; 0 U; 0 Other;

Query Match             99.7%;  Score 1150.8; DB 12;  Length 1154;
Best Local Similarity   99.8%;  Pred. No. 1.7e-273;
Matches 1152;   Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCGGCCCTACCTCGCCCGAGCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCGGCCCTACCTCGCCCGAGCGCC 60

Qy    61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTTCCCGCTGGGCCGAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTTCCCGCTGGGCCGAGCAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGAGCCCGCACATCTCCCGCCATCCGGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGAGCCCGCACATCTCCCGCCATCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACGGTGACATTGCCGTG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACGGTGACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCGTCCTC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCGCTCAAGAGCGTCCAAGAGCGTCCGGCTCCTTTCT 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACCCTGATGATCCGCTCAAGAGCGTCCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG 840
```

CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one additive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C1008T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity   99.8%; Pred. No. 1.7e-273;
Matches 1152; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGAGCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCGGCCGAGCCGGCCGAGCCGGCCGACAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCGGCCGAGCCGGCCGAGCCGGCCGACAGCAGCAACGGC 120

Qy 121 AGCGGCCGGTCGGAGGACGCGGCAGCTGGAGCCGGCAGCGGCCGGCATCCCGGCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGCGGCCGGTCGGAGGACGCGGCAGCTGGAGCCGGCAGCGGCCGGCATCCCGGCATCCCGGTC 180

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCCAACTCGCTGGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCCAACTCGCTGGTC 240

Qy 241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCAGCAACCAACATTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCAGCAACCAACATTACATATTTAAC 300

Qy 301 CTGGCTTGGCCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CTGGCTTGGCCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTG 360

Qy 361 ATGAATTCCTGGCCTTTTGGGGATGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 ATGAATTCCTGGCCTTTTGGGGATGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy 421 AACATGTTCACCAGCATCTTGACCATGGACCGTACATTGCCGTG 480
         |||||||||||||||||||||||||||||||||||||||||||
Db 421 AACATGTTCACCAGCATCTTGACCATGGACCGTACATTGCCGTG 480

Qy 481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGCAAGATCATCAATATC 540
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db 481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGCAAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTGCGTCATCGTTGGCATCCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy 841 GCAGTCTTCGTTGCTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
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Db 841 GCGGTCTTCGTTGCTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACCTCCCACAGCACAGCAGTCGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 AGCACCTCCCACAGCACAGCAGTCGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy 961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGAGCGGCAGCGACCAGCACTAGCAGAGTC 1080
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Db 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGAGCGGCAGCGACCAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAAACCAGTA 1140
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Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGATGAATAAAACCAGTA 1140

Qy 1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db 1141 TGACTAGTCGTGGA 1154

RESULT 5
ADN30508
ID   ADN30508 standard; cDNA; 1154 BP.
XX
AC   ADN30508;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C1008T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity,; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   allele   replace(1008,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 4; 29pp; English.
XX

XX
PF　13-JUL-2001; 2001US-00904584.
XX
PR　14-JUL-2000; 2000US-0218300P.
XX
PA　(KREE/) KREEK M J.
PA　(YUFE/) YUFEROV V.
PA　(LAFO/) LAFORGE K S.
XX
PI　Kreek MJ, Yuferov V, Laforge KS;
XX
DR　WPI; 2004-389204/36.
XX
PT　Novel isolated variant allele of human kappa opioid receptor gene, useful
PT　for determining susceptibility in subject to physiological response,
PT　condition or disease related to endogenous opioid system.
XX
PS　Example; SEQ ID NO 3; 29pp; English.
XX
CC　The invention relates to an isolated variant allele of a human kappa
CC　opioid receptor gene, comprising a DNA sequence having at least one
CC　variation in a fully defined wild-type allele of human kappa opioid
CC　receptor (hKOR) sequence appearing as ADN30505, where the variation
CC　comprises C852T, C1008T or their combinations. Also included are
CC　an isolated nucleic acid molecule selectively hybridising to the variant,
CC　a cloning vector comprising the variant and an origin of replication, an
CC　expression vector comprising the variant associated with a promoter, a
CC　unicellular host transformed/transfected with the vector and a commercial
CC　test kit for determining the presence of at least one variation in a hKOR
CC　gene of an allele in a bodily sample taken from a subject. The hKOR
CC　variant allele is useful for determining a susceptibility in a subject to
CC　at least one physiological response, condition or disease related to the
CC　endogenous opioid system, nociception, neurotransmitter release
CC　endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC　amphetamine and other stimulants self-administration, behavioural
CC　sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC　amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC　neuroendocrine function, reproductive function, prolactin regulation,
CC　stress responsivity, physiology and pathology of mood and affect, immune
CC　function, gastrointestinal function. The hKOR variant allele is useful
CC　for determining a susceptibility to pain in a subject and is useful for
CC　determining a therapeutically effective amount of pain reliever to
CC　administer to a subject in order to induce analgesia in the subject. The
CC　hKOR variant allele is useful for determining a therapeutically effective
CC　amount of therapeutic agent to administer to a subject suffering from at
CC　least one addictive disease to treat the at least one additive disease.
CC　The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC　is the C948T allele of hKOR.
XX
SQ　Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match　99.7%;　Score 1150.8;　DB 12;　Length 1154;
Best Local Similarity　99.8%;　Pred. No. 1.7e-273;
Matches 1152;　Conservative　0;　Mismatches　2;　Indels　0;　Gaps　0;

Qy　　1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCCTACCTGCGCCCCAGCGCC 60
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCCTACCTGCGCCCCAGCGCC 60

Qy　 61 TGCCTGCCCCCAACAGCAGCCCTGGTTTCCCGGCTGGCCGGGCACCAGCAGCAACGGC 120
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　 61 TGCCTGCCCCCAACAGCAGCCCTGGTTTCCCGGCTGGCCGGGCACCAGCAGCAACGGC 120

Qy　121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCGCGGTGGC 180
　　　　||||||||||||||||||||||||||||||||||||||||
Db　121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCGCACCATCCGGGTC 180

Qy　181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTC 240
　　　　||||||||||||||||||||||||||||||||||||||||
Db　181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTCGGCAACTCGGTC 240

Qy　241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACATTTACATATTTAAC 300

Db　541 TGCATCTGGCTGCTCGTCGTCATCTTGTGGCAATAGTCCTTGGAGGCACCAAA 600
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　601 GTCAGGAAGAGACTCGATGTCATTGAGTGCAGTTCCCAGATGATGACTACTCC 660
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　601 GTCAGGAAGAGACTCGATGTCATTGAGTGCAGTTCCCAGATGATGACTACTCC 660

Qy　661 TGGTGGGACCTTCATGAAGATCTGCGTCTCATCTTTGCCTTCGTGATCCTCCTC 720
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　661 TGGTGGGACCTTCATGAAGATCTGCGTCTCATCTTTGCCTTCGTGATCCTCCTC 720

Qy　721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGGTCCGGCTCCTTCT 780
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGGTCCGGCTCCTTCT 780

Qy　781 GGCTCCCCAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGTCCTGTGGTGGTG 840
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　781 GGCTCCCCAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGTCCTGTGGTGGTG 840

Qy　841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy　901 AGCACCTCCCACAGCACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTAGGCTAT 960
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　901 AGCACCTCCCACAGCACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTAGGCTAT 960

Qy　961 ACCAACAGTAGCCTAGACTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　961 ACCAACAGTAGCCTAGACTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020

Qy　1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGGCAGAGCACTAGCAGAGTC 1080
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Db　1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGGCAGAGCACTAGCAGAGTC 1080

Qy　1081 CGAAATACAGTTCAGGATTCGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1140
　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1081 CGAAATACAGTTCAGGATCCTGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy　1141 TGACTAGTCGTGGA 1154
　　　　||||||||||||||
Db　1141 TGACTAGTCGTGGA 1154

RESULT 6
ADN30507
ID　ADN30507　standard; cDNA; 1154 BP.
XX
AC　ADN30507;
XX
DT　12-AUG-2004　(first entry)
XX
DE　Human kappa opioid receptor, hKOR, C948T allele.
XX
KW　Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW　single nucleotide polymorphism; endogenous opioid system; nociception;
KW　neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW　amphetamine; alcohol; tobacco; opiate; withdrawal;
KW　neuroendocrine function; reproductive function; prolactin regulation;
KW　stress responsivity.; mood; affect; immune function;
KW　gastrointestinal function; analgesia; additive disease;
KW　chromosome 8q11.2.
XX
OS　Homo sapiens.
XX
FH　Key　Location/Qualifiers
FT　allele　replace(948,C)
FT　　　　　/tag= a
FT　　　　　/standard_name= "Single nucleotide polymorphism"
XX
PN　US2004097704-A1.
XX
PD　20-MAY-2004.

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Qy   241  ATGTTCGTGATCATCCGATACACAAGATGAAGACAGCAACCACATTTACATATTTAAC  300

Db   301  CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301  CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Db   361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420

Qy   421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
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Db   421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy   481  TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Db   481  TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy   541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA  600
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Db   541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA  600

Qy   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Db   661  TGGTTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720

Qy   721  ATCATCATCTGTCTGTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATCATCATCTGTCTGTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTTGGTGGTGGTG  840

Qy   841  GCAGTCTTCGTTGCTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCAGTCTTCGTTGCTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGG  900

Qy   901  AGCACCTCCCACAGCACAGTCGCTATTACTTCTGCATCGGCTATTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AGCACCTCCCACAGCACAGTCGCTATTACTTCTGCATCGGCTATTAGGCTAT  960

Qy   961  ACCAACAGTAGCCTGAATCCCATTCCTACGCGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  ACCAACAGTAGCCTGAATCCCATTCCTACGCGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy   1021  TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC  1080

Qy   1081  CGAAATACAGTCAGATCTCAGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAAATACAGTCAGATCTCAGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141  TGACTAGTCGTGGA  1154
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Db   1141  TGACTAGTCGTGGA  1154
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RESULT 7

ADN30511

ID ADN30511   standard; cDNA; 1154 BP.
XX
AC ADN30511;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human kappa opioid receptor, hKOR, C856T allele.
XX

KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW single nucleotide polymorphism; endogenous opioid system; nociception;
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW amphetamine; alcohol; tobacco; opiate; withdrawal;
KW neuroendocrine function; reproductive function; prolactin regulation;
KW stress responsivity,; mood; affect; immune function;
KW gastrointestinal function; analgesia; additive disease;
KW chromosome 8q11.2.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT allele   replace(846,C)
FT   /tag= a
FT   /standard_name= "single nucleotide polymorphism"
XX
PN US2004097704-A1.
XX
PD 20-MAY-2004.
XX
PF 13-JUL-2001; 2001US-00904584.
XX
PR 14-JUL-2000; 2000US-0218300P.
XX
PA (KREE/) KREEK M J.
PA (YUFE/) YUFEROV V.
PA (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, Yuferov V, Laforge KS;
XX
DR WPI; 2004-389204/36.
XX
PT Novel isolated variant allele of human kappa opioid receptor gene, useful
PT for determining susceptibility in subject to physiological response,
PT condition or disease related to endogenous opioid system.
XX
PS Example; SEQ ID NO 7; 29pp; English.
XX
CC The invention relates to an isolated variant allele of a human kappa
CC opioid receptor gene, comprising a DNA sequence having at least one
CC variation in a fully defined wild-type allele of human kappa opioid
CC receptor (hKOR) sequence appearing as ADN30505, where the variation
CC comprises C852T, C948T, C1008T or their combinations. Also included are
CC an isolated nucleic acid molecule selectively hybridising to the variant,
CC a cloning vector comprising the variant and an origin of replication, an
CC expression vector comprising the variant associated with a promoter, a
CC unicellular host transformed/transfected with the vector and a commercial
CC test kit for determining the presence of at least one variation in a hKOR
CC gene of an allele in a bodily sample taken from a subject. The hKOR
CC variant allele is useful for determining a susceptibility in a subject to
CC at least one physiological response, condition or disease related to the
CC endogenous opioid system, nociception, neurotransmitter release
CC endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC amphetamine and other stimulants self-administration, behavioural
CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC neuroendocrine function, reproductive function, prolactin regulation,
CC stress responsivity, physiology and pathology of mood and affect, immune
CC function, gastrointestinal function. The hKOR variant allele is useful
CC for determining a susceptibility to pain in a subject and is useful for
CC determining a therapeutic effective amount of pain reliever to
CC administer to a subject in order to induce analgesia in the subject. The
CC hKOR variant allele is useful for determining a therapeutically effective
CC amount of therapeutic agent to administer to a subject suffering from at
CC least one addictive disease to treat the at least one additive disease.
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC is the C846T allele of hKOR.
XX
SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity 99.8%; Pred. No. 1.7e-273;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC  60

Qy   61 TGCCTGCCCCAACAGCAGCGGCCTGGTTCCCGGCCGGAGCCGACAGCAACGGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCAACAGCAGCGGCCTGTTCCCGGCCGGAGCCGACAGCAACGGC 120

Qy  121 AGCGCCGGCTCGGAGGACGCGCCAGCTGGAGCCGCGCACATCTCCCCGGCCATCCCGGTC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGCGCCGGCTCGGAGGACGCGCCAGCTGGAGCCGCGCACAATCTCCCCGGCCATCCCGGTC 180

Qy  181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGGTGGCAACTCGCTGGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGGTGGCAACTCGCTGGTC 240

Qy  241 ATGTTCGTGATCATCCGATACACAACAAAGATGAAGACAGCAACAATTTACATATTTAAC 300
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Db  241 ATGTTCGTGATCATCCGATACACAACAAAGATGAAGACAGCAACAATTTACATATTTAAC 300

Qy  301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTGTGCAAGATAGTAATTCCATTGATTACTAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTGGGGATGTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGGTGGACCGTCACATTGCGTG 480
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Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGGTGGACCGTCACATTGCCGTG 480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy  541 TGCATCTGGCTGCTCGTCGTCATCTGTTGGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTCGTCGTCATCTGTTGGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCGTCCTTGCAGTTCCCAGTGACTACTCC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCGTCCTTGCAGTTCCCAGTGACTACTCC 660

Qy  661 TGGTGGACCCTTTCATGAAGATCTGCGTCTTCATCTTGCTGTGATCCCGTCCTC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGACCCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGGATCGGTCCTGGTGGTG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGGATCGGTCCTGGTGGTG 840

Qy  841 GCAGCTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTTTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGTGGAGGCTCTGGGG 900

Qy  901 AGCACCTTCCACAGCACAGCTCGTCTCTTCCAGCTATTACTTCTGCCTTAGGCTAT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGCACCTTCCCACAGCACAGCTGCTCTCTCCAGCTATTTCTGCCTTAGGCTAT 960

Qy  961 ACCAAGACTAGCCTGAATCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGGAGTGT 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAAGACTAGCCTGAATCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCCGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGCGCAGAGCCACTAGCAGAGTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGCAGAGCCACTAGCAGAGTC 1080
```

```
Qy 1081 CGAAATACAGTTCAGGATCGTCGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
        |||||||||||||||||||        |||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy 1141 TGACTAGTCGTGA 1154
        |||||||||||||
Db 1141 TGACTAGTCGTGA 1154
```

```
RESULT 8
ADN30509
ID   ADN30509    standard; cDNA; 1154 BP.
XX
AC   ADN30509;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, G36T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key                 Location/Qualifiers
FT   allele              replace(36,G)
FT                       /*tag= a
FT                       /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 5; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
```

```
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the G36T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 286 G; 339 C; 290 T; 0 U; 0 Other;

Query Match             99.7%;  Score 1150.8;  DB 12;  Length 1154;
Best Local Similarity   99.8%;  Pred. No. 1.7e-273;
Matches 1152;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy       61 TGCCTGCCCCCAACAGCAGGGCCTGGTTTCCCGGCCTGGGCCGAGCCCGACAGCAACGGC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTGCCCCCAACAGCAGCGCCTGTGTTTCCCGGCCTGGGCCGAGCCCGACAGCAACGGC 120

Qy      121 AGCGGCCGGCTCGGAGGACGCGGCCAGCTGGAGCCCCGGCCACATCTCCCCGGCCATCCGGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCGGCCGGCTCGGAGGACGCGGCCAGCTGGAGCCCCGGCCACATCTCCCCGGCCATCCGGGTC 180

Qy      181 ATCATCACGGCGGGGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCAACTCGCTGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ATCATCACGGCGGGGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy      241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAACATATTTAAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAACATATTTAAC 300

Qy      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy      361 ATGAATTCCTGGCCTTTTGGGGATGTGCGTGTGCAAGATAAATTTCCATTGATTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATGAATTCCTGGCCTTTTGGGGATGTGCGTGTGCAAGATAGTAAATTTCCATTGATTACTAC 420

Qy      421 AACATGTTCACCAGCATCTTCACCTTGACTGTGAGCGTGGACCGCTACATTGCCGTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AACATGTTCACCAGCATCTTCACCTTGACTGTGAGCGTGGACCGCTACATTGCCGTG 480

Qy      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy      541 TGCATCTGGCTGCTGTCGTCATCCGTATCTGGCAATAGTCCTTGGAGGCACCAAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGCATCTGGCTGCTGTCGTCATCCGTATCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy      601 GTCAGGGAAGACCTGCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCAGGGAAGACCTGCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy      661 TGGTGGGACCTTCATGATGAAGATCTGCGTCTTCATCTTTGCCTTGCTTCGTGATCCCTGTCCTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGGTGGGACCTTCATGATGAAGATCTGCGTCTTCATCTTTGCCTTGCTTCGTGATCCCTGTCCTC 720

Qy      721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCGGCTCCTTTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCGGCTCCTTTCT 780

Qy      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCACCAGACTGGTCCTGGTGGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCACCAGACTGGTCCTGGTGGTG 840

Qy      841 GCAGTCTTCGTCGTCGTCGTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCAGTCTTCGTCGTCGTCGTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy      901 AGCACCTCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AGCACCTCCACACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy      961 ACCAACAGTAGCCTGAATCCCATTCCTTACGCCCTTTCTTCTTGATGAAAACTTCAAGCGGTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACAGTAGCCTGAATCCCATTCCTTACGCCCTTTCTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy     1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGATGAGCGGCAGAGCACTAGCAGAGTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGATGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy     1141 TGACTAGTCGTGGA 1154
            ||||||||||||||
Db     1141 TGACTAGTCGTGGA 1154
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RESULT 9

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AB242678
ID   AB242678 standard; DNA; 1182 BP.
XX
AC   AB242678;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20026l087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC, Roush CL, Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81832.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
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XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match             99.2%;  Score 1144.4;  DB 8;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 6.4e-272;
Matches  1148;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGACTCCCCGATCCAGATCTTCCGCGGGAGCCGGGCCGGGCCCTACCTGCGCCCCGAGCGCGCC 60
              ||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGGAATCCCCGATTCAGATCTTCCGCGGGAGCCGGGCCGGGCCCTACCTGCGCCCCGAGCGCGCC 73

Qy         61 TGCCTGCCCCCCAACAGCAGCCGGCTCGGCCAGCTGGGCCCGGTTTCCCGGCCCGAGCCGACAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 TGCCTGCCCCCCAACAGCAGCCGGCTCGGCCAGCTGGGCCCGGTTTCCCGGCCCGAGCCGACAGCAACGGC 133

Qy        121 AGCGCCGGCTCGGAGGACGCGCGCAGCTGGACCTGGAGCCCATCTCCCCGGCCCATCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 AGCGCCGGCTCGGAGGACGCGCGCAGCTGGACCTGGAGCCCATCTCCCCGGCCCATCCCGGTC 193

Qy        181 ATCATCACGGGGGTCTCACTCCGTAGTGTTCGTGCGTGGGCTTGGTGGGCCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 ATCATCACGGGGGTCTCACTCCGTAGTGTTCGTGCGTGGGCTTGGTGGGCCAACTCGCTGGTC 253

Qy        241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAAC 313

Qy        301 CTGGCTTTGGCAGATGCTTTAGTTGCTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 CTGGCTTTGGCAGATGCTTTAGTTGCTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 433

Qy        421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493

Qy        481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy        541 TGCATCTGGCTGCTGTCGTCATCCGTATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 TGCATCTGGCTGCTGTCGTCATCCGTATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613
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```
Qy        601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTGCTTCCTTGAGTGATGACTACTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTGCTTCCTTGAGTGATGACTACTCC 673

Qy        661 TGGTGGGACCTCTTCATGAAGATCTGCCGTCTTCATCTTGCCTTCGTCTTCGTCCCTGTCCTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 TGGTGGGACCTCTTCATGAAGATCTGCCGTCTTCATCTTGCCTTCGTCTTCGTCCCTGTCCTC 733

Qy        721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCCTTTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCCTTTCT 793

Qy        781 GGCTCCCAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 GGCTCCCAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy        841 GCAGTCTTCGTTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTTCTGGGG 900
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 GCGGTTTTCGTTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTTCTGGGG 913

Qy        901 AGCACCTCCCAGCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGCACCTCCCAGCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 973

Qy        961 ACCAACAGTAGCCTGAATCCCATTCTTCACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ACCAACAGTAGCCTGAATCCCATTCTTCACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1033

Qy       1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGTGCGGCGCAGAGCACTAGCAGAGTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGTGCGGCGCAGAGCACTAGCAGAGTC 1093

Qy       1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy       1141 TGACTAGTCGTGGA 1154
              ||||||||||||||
Db       1154 TGACTAGTCGTGGA 1167
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RESULT 10
AAD58490
ID   AAD58490 standard; DNA; 1182 BP.
XX
AC   AAD58490;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human kappa opioid receptor 1 (KOR) DNA.
XX
KW   Human; urological disorder; urinary incontinence; gene therapy; cancer;
KW   kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
KW   urethra; overflow urinary incontinence; stress urinary incontinence;
KW   nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
KW   kappa opioid receptor 1; KOR; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             14..1156
FT                   /tag= a
FT                   /product= "Human kappa opioid receptor 1 (KOR)"
FT                   /note="The CDS is referred to as SEQ ID NO:21 in the
FT                   specification"
XX
PN   WO2003061573-A2.
XX
PD   31-JUL-2003.
XX
PF   16-JAN-2003; 2003WO-US001450.
XX
PR   18-JAN-2002; 2002US-0349511P.
```

PR 28-FEB-2002; 2002US-0360500P.
PR 15-MAR-2002; 2002US-0365041P.
PR 19-APR-2002; 2002US-0374063P.
PR 14-AUG-2002; 2002US-0403468P.
PR 27-SEP-2002; 2002US-0414262P.
PR 21-OCT-2002; 2002US-0419986P.
PR 05-NOV-2002; 2002US-0423809P.
PR 26-NOV-2002; 2002US-0429797P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Silos-Santiago I, Karicheti V;
XX
DR WPI; 2003-598705/56.
DR P-PSDB; AAE38589.
XX
PT Identifying a compound for treating urological disorders, for example
PT urinary incontinence by assaying the ability of the compound to modulate
PT the nucleic acid expression or polypeptide activity.
XX
PS Disclosure; Page 149-151; Opp; English.
XX
CC The present relates to a method for identifying a compound for treating
CC urological disorders e.g., urinary incontinence including overactive/
CC oversensitive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central or
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC cancer of the prostate or kidney disorders. The method is also useful for
CC modulating hyperplasia in a cell and treating a subject having a
CC urological disorder. The invention is also used in gene therapy. The
CC present sequence is human kappa opioid receptor 1 (KOR) DNA
XX
SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match   99.2%; Score 1144.4; DB 10; Length 1182;
Best Local Similarity 99.5%; Pred. No. 6.4e-272;
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGAGCCCTACCTGCCTGCGCCCGAGCGCC 60
          ||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGAGCCCTACCTGCCTGCGCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCAACAGCAGGGCCTGGTTCCGGTGGGCGGAGCAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCAACAGCAGCAGCGGCCTGGTTCCGGTGGGCGGAGCAGCAACGGC 133

Qy   121 AGGGCCGGCTCGGAGGACGGGGCAGCTGGAGCGGCACATCTCCCCGGCCATCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGGGCCGGCTCGGAGGACGGGGCAGCTGGAGCGGCACATCTCCCCGGCCATCCGGTC 193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGCTTGGTGGGCAACTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATCACCCTTTCAGAGTACGGTCTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTCAAGATAGTAATTTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGAACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGAACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTTCTGCTGGCATCTCTGTTGGCATCTCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTTCTGCTGGCATCTCTGTTGGCATCTCTG 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCAGTTCCCGAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTGCCTTCGTGATCCCGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTGCCTTCGTGATCCCGTCCTC 733

Qy   721 ATCATCATCGTCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCGTCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 793

Qy   781 GGCTTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCACGACTGGTCCGGTCGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCACGACTGGTCCGGTCGGTGGTG 853

Qy   841 GCAGTCTTCGTTGTGTGCTGGACTCCCATTCACATAATTCATCCTGGTGGAGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTTCGTCGTGCTGCTGGACTCCCATTCACATAATTCATCCTGGTGGAGGCTCTGGGG 913

Qy   901 AGCACCTCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCTGCAATCCCATTCCATTCCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCCATTCCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCGGGACTTCTGCTTCGTCTTCCACTGAAGATCGGCGGCAGAGCACTAGACAGAGTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCGGGACTTCTGCTTCGTCTTCCACTGAAGATGAGGATGGAGACGGCAGAGCACTAGACAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1154 TGACTAGTCGTGGA 1167

RESULT 11
ADE84861
ID ADE84861 standard; DNA; 1182 BP.
XX
AC ADE84861;
XX
DT 29-JAN-2004 (first entry)
XX
DE Farnesyl transferase inhibitor modulated leukemia associated gene #80.
XX
KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW quinolinone; leukemia; cancer.
OS Homo sapiens.
XX
PN WO200303129-A2.
XX
PD 08-MAY-2003.
XX
PF 30-OCT-2002; 2002WO-US034784.
XX
PR 30-OCT-2001; 2001US-0338997P.
PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

```
XX
PI   Raponi M;
XX
DR   WPI; 2003-513497/48.
XX
PT   Determining whether a patient will respond to treatment with a farnesyl
PT   transferase inhibitor, by analyzing the expression of gene that is
PT   differentially modulated in the presence of the inhibitor.
XX
PS   Disclosure; SEQ ID NO 80; 346pp; English.
XX
CC   The invention relates to a method of determining whether a patient will
CC   respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC   analyzing the expression of gene that is differentially modulated in the
CC   presence of an FTI. The method is useful for determining whether a
CC   patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC   chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC   methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC   patient with leukemia with FTI if the analysis indicates that the patient
CC   will respond. This sequence corresponds to a gene whose expression may be
CC   modulated in the presence of FTI.
XX
SQ   Sequence 1182 BP; 245 A; 293 C; 345 G; 299 T; 0 U; 0 Other;

Query Match             99.2%;  Score 1144.4;  DB 10;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 6.4e-272;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy     1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTTACCTGCCCCGAGCGCC 60
           |||||||||||| ||||||||||||||||||||| |||||||| |||||| |||||||||
Db    14 ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCTGGGCCCTACCTGCGCCCGAGCGGCC 73

Qy    61 TGCCTGCCCCCAACAGCAGCGCGTCGGTTTCCCGGCGCCGAGCCCGAGCACGACGGC 120
           |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db    74 TGCCTGCCCCCAACAGCAGCGCCTCGGTTTCCCGGCGCCGAGCCCGAGCAGCAGCAACGGC 133

Qy   121 AGCGGCGGCTCGGAGGACGCGGCCAGCTGGAGCCCGCCGCACATCTCCCGGCCATCCCGGTC 180
           |||||||||||||||||||||||| |||||||||||||||||||||| |||||||||||||
Db   134 AGCGGCCGGCTCGGAGGACGCGGCCAGCTGGAGCCCGCCGCACATCTCCCGGCCATCCCGGTC 193

Qy   181 ATCATCACGGCCGTCTACTCCGTCAGTGTTCGTCGTGTGGGCTTGCTGCTGCTGC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGCGTCTACTCCGTCAGTGTTCGTCGTGTTCGTGGGCTTGCTGCTGCTGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCAACATGCCCTTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTAGTTACTACAACCAACATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGGCGGTGGACCGTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGGCGGTGGACCGTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTCGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTCGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACTCCTTCTTCATGAAGATCTGGCGTCTTCCATCTTCGTCTTGCCTCGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACTCCTTCTTCATGAAGATCTGGCGTCTTCCATCTTCGTCTTGCCTCGTCCTC 733

Qy   721 ATCATCATCGTCTGCTACACCCTGCTGTCTTCAAGAGGCGTCCGGCGTCCGGCTCCTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACACCCTGCTGTCTTCAAGAGGCGTCCGGCGTCCGGCTCCTTCT 793

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTGGTCCTGGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTGGTCCTGGTGGTG 853

Qy   841 GCAGTCTCCTGTCTGCTGGACTCCCATTCACATATTCATCCTCGGTGGAGGCTCTCGGGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGG 913

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy  1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGGGACACTAGCAGAGTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGGGACACTAGCAGAGTC 1093

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy  1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db  1154 TGACTAGTCGTGGA 1167


RESULT 12
ACA56819
ID   ACA56819 standard; cDNA; 1182 BP.
XX
AC   ACA56819;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1417.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
PF   30-JAN-1998;  98US-00016434.
XX
PR   30-JAN-1998;  98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J, Seilhamer JJ;
XX
DR   WPI; 2003-352189/33.
XX
PT   Combination of polynucleotide probes, useful as array elements in a
PT   microarray for monitoring the expression of a number of target
PT   polynucleotides.
XX
PS   Claim 1; SEQ ID NO 1417; 65pp; English.
XX
CC   The invention relates to a combination which, comprises a number of
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CC   polynucleotide probes comprising a sequence selected from one of the 1490
CC   sequences mentioned in the specification. The combination is useful as an
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note:The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match             99.2%;  Score 1114.4;  DB 10;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 6.4e-272;
Matches 1148;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCGGCCCTACCTGCGCCCCGAGCGCC   60
          ||||| | |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGGCCGGCCCTACCTGCGCCCCGAGCGCC   73

Qy     61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC  133

Qy    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGACGCCGGCACATCTCCCCGGCCATCCCGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AGCGCCGGCTCGGAGGACGCGCAGCTGGACGCCGGCACATCTCCCCGGCCATCCCGGTC  193

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCGGCTTGGTGGGCAACTCGCTGGTC  240
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 ATCATCACGGGGGTCTACTCCGTAGTGTTCGTCGTGGCGGCTTGGTGGGCAACTCGCTGGTC  253

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  313

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  373

Qy    361 ATGAATTCCTGGCCTTTGGGGATGCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ATGAATTCCTGGCCTTTGGGGATGCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC  433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACACATTGCCGTG  493

Qy    481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  553

Qy    541 TGCATCTGGCTGCTCGTCATCTGGCATCCTTGCAATAGTCCTTGGAGGCACCAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTGGCTGCTCGTCATCTGGCATCCTTGCAATAGTCCTTGGAGGCACCAAA  613

Qy    601 GTCAGGGAAGACGTCGATGTCATTGCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAAGACGTCGATGTCATTGCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  673

Qy    661 TGGTGGGACCTTCATGAAGATCTGCTTCTCATCTTTGCCTCTTTGCCTTCGATCCCGTGTCCTC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTTCATGAAGATCTGGCGTCTTCATCTTTGCCTTCGTGTCCGTGATCCCGTCCTC  733

Qy    721 ATCATCACTGCTCGCTACACCCTGATGATCTGCGGCTCCAAGAGCGTCCAAGAGGGCTCCTTTCT  780
          ||||||||| || |||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    734 ATCATCACTCTCTGCTACACCCTGATGATCTGCGGCTCCAAGAGGGCTCCAAGAGGGCTCCTTTCT  793

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  853

Qy    841 GCAGTCTTCGTTGTCTGGACTCCCCATTCACATATTCATCCTCGGTGGAGGCTTGGGGG  900
          || ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 GCGGTTTTCGTTGTCTGGACTCCCCATTCACATATTCATCCTCGGTGGAGGCTTGGGGG  913

Qy    901 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  973

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTCGCTTCCACTGAAGATGGAGGATGGAGCGCAGCACTAGCAGAGTC 1080
          |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGCAGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCGTGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCGTGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1154 TGACTAGTCGTGGA 1167


RESULT 13
ADI56615
ID   ADI56615 standard; DNA; 1182 BP.
XX
AC   ADI56615;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human polynucleotide probe #1417.
XX
KW   Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW   effector-like polypeptide; cancer; immunopathology; neuropathology;
KW   drug development; toxicology; carcinogenicity;
KW   signalling pathway polypeptide; adrenal gland; bladder; bone;
KW   bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW   diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW   dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS   Homo sapiens.
XX
PN   US2004010136-A1.
XX
PD   15-JAN-2004.
XX
PF   26-NOV-2002; 2002US-00305720.
XX
PR   30-JAN-1998;  98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J, Seilhamer JJ;
XX
DR   WPI; 2004-090520/09.
XX
PT   New composition comprising polynucleotide probes, useful as array
PT   elements in a microarray for monitoring the expression of target
PT   polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
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PT
XX
PS   Claim 6; SEQ ID NO 1417; 73pp; English.
XX
CC   The invention relates to a composition of polynucleotide probes
CC   comprising first polynucleotide probes comprising at least a portion of a
CC   gene encoding a receptor-like polypeptide, second polynucleotide probes
CC   comprising at least a portion of a gene encoding a transducing
CC   polypeptide and third polynucleotide probes comprising at least a portion
CC   of a gene encoding an effector-like polypeptide. The probes of the
CC   composition are useful as array elements in a microarray for monitoring
CC   the expression of target polynucleotides. The microarray is useful in the
CC   diagnosis and treatment of cancer, an immunopathology or a
CC   neuropathology. It can also be used for drug discovery and development,
CC   toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC   Microarrays can also be used for monitoring the progression of diseases
CC   that may be associated with the altered expression of signalling pathway
CC   polypeptides. The composition can also be used to purify a subpopulation
CC   of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC   is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC   the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC   an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC   ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC   epilepsy, Alzheimer's disease or depression. This sequence represents a
CC   human polynucleotide probe of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match             99.2%;  Score 1144.4;  DB 12;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 6.4e-272;
Matches  1148;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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```
Qy      1 ATGGACTCCCCGATCCCAGATCTTCCGCGGGGAGCCCGGCGCCCTTACCTGCGCCCGAGCGCC  60
          ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCCGGCGCCCTTACCTGCGCCCGAGCGCC  73

Qy     61 TGCCTGCCCCCAACAGCAGCGGCGGCCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 TGCCTGCCCCCAACAGCAGCGGCGGCCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 133

Qy    121 AGCGCCGGCTCGGAGGACGCGGCAGTCGGAGCCGCGCGCACATCTCCCCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AGCGCCGGCTCGGAGGACGCGGCAGTCGGAGCCGCGCGCACATCTCCCCGGCCATCCCGGTC 193

Qy    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy    241 ATGTTCGTGATCATCCGATACCAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ATGTTCGTGATCATCCGATACCAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy    301 CTGGCTTTGGCAGATGTGCTTTAGTTACTACAACCATGCCCTTTCAGATACCGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 CTGGCTTTGGCAGATGTGCTTTAGTTACTACAACCATGCCCTTTCAGATACCGGTCTACTTG 373

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTCAAGATAGTAATTTCCATTGATTACTAC 433

Qy    421 AACATGTTCACCCAGCATCTTCACCTTGACCATGAGCGTTGACCCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AACATGTTCACCCAGCATCTTCACCTTGACCATGAGCGTTGACCCGCTACATTGCCGTG 493

Qy    481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTGGCTGCTCGTGTCGTCATCTGTTGGCATCTCTGGAGGCACCAAA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTGGCTGCTCGTGTCGTCATCTGTTGGCATCTCTGGAGGCACCAAA  613

Qy    601 GTCAGGGAGGAAGACGTCGGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGAGTGACTACTCC 660
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAGGAAGACGTGCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGAGTGACTACTCC 673

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGGCGTCTTCATCTTGCCTTGCCTTCGTCGATCCCTGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTCTTCATGAAGATCTGGCGTCTTCATCTTGCCTTGCCTTCGTCGATCCCTGTCCTC 733

Qy    721 ATCATCATCGTCTGCTACACACCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 ATCATCATCGTCTGCTACACACCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 793

Qy    781 GGCTCCCAGAGAAAGATCGCAACCTGGCTAGGATCCACCAGACTGGTCTCTGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCCAGAGAAAGATCGCAACCTGGCTAGGATCCACCAGACTGGTCTCTGGTGGTGGTG 853

Qy    841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 913

Qy    901 AGCACCTCCCAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AGCACCTCCCAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCCATTTCTTCTGATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 ACCAACAGTAGCCTGAATCCCATTCCCATTTCTTCTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGATGGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGATGGCGGCAGAGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATACTCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGA 1154
          |||||||||||||
Db   1154 TGACTAGTCGTGA 1167
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RESULT 14
AAT90998
ID   AAT90998 standard; cDNA; 1143 BP.
XX
AC   AAT90998;
XX
DT   14-APR-1998  (first entry)
XX
DE   Human kappa opioid receptor cDNA.
XX
KW   Selective target cell activation; G protein-coupled receptor; RASSL;
KW   gene therapy; cell proliferation; kappa opioid receptor; human;
KW   transgenic animal; arrhythmia; bone disease; seizure;
KW   vascular contraction; disease model; ss.
XX
OS   Homo sapiens.
XX
PN   WO9735478-A1.
XX
PD   02-OCT-1997.
XX
PF   25-MAR-1997;  97WO-US005334.
XX
PR   26-MAR-1996;  96US-00622348.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Conklin BR;
XX
DR   WPI; 1997-502739/46.
```

DR   P-PSDB; AAW30297.
XX
PT   Selective activation of target cell expressing modified G protein coupled
PT   receptor - allows control of cellular proliferation, especially for
PT   amplification of transfected cells in gene therapy.
XX
PS   Example 1; Page 74-76; 117pp; English.
XX
CC   This cDNA sequence comprises the coding region for human kappa opioid
CC   receptor (KOR, see AAW30297), a G protein-coupled receptor implicated in
CC   neurotransmission. A novel method for selectively activating a target
CC   cell (TC) comprises: (i) introducing into the cell a nucleic acid
CC   sequence (I) that expresses a G protein-coupled receptor (A) modified to
CC   be activated superiorly by a synthetic ligand (RASSL); and (ii) exposing
CC   the transfected cell to small synthetic molecules (B) that bind to and
CC   activate (A), inducing the G protein coupled cellular response associated
CC   with receptor activation. (A) has: (a) decreased binding affinity for a
CC   selected natural ligand of the native receptor; (b) binding affinity for
CC   (B); and (c) is activated by binding (B) sufficiently to produce the
CC   required cellular response. Also new are: (1) transgenic cells including
CC   heterologous (I) in the genome; (2) cellular implants comprising a TC
CC   transfected with (I); (3) isolated (I); and (4) transgenic non-human
CC   animals expressing (A). Activation of (A) results, in vitro or in vivo,
CC   in cellular proliferation, or secretion of a cellular product,
CC   particularly a heterologous therapeutic protein encoded by a second
CC   inserted nucleic acid sequence. Particularly it is used to expand the
CC   relatively few cells that are successfully transfected during cell
CC   therapy procedures. Other responses that can be regulated are cell
CC   migration and contraction, or pigment production. In transgenic animals,
CC   expression or stimulation of (A) is designed to develop cardiac
CC   arrhythmia, symptoms of bone disease, seizures, vascular contractions,
CC   dementia, neurodegeneration etc., for use as models of these diseases
CC   (claimed). The transgenic animals are also used for production of
CC   improved food products (e.g. increased calcium content in eggshells or
CC   altered fat/lean ratios) or to control fertility or induce labour. A
CC   RASSL derived from KOR, designated RASSL OR1 (see AAW30299), was
CC   generated by mutation of the KOR cDNA sequence.
XX
SQ   Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match   98.9%;
Best Local Similarity   99.9%;
Matches 1142;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

```
Qy      1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy     61 TGCCTGCCCCCAAACAGCAGGGCCTTCCGGTTTCCCGGCTGGGCCGGAGCCCGACAGCGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAAACAGCAGGGCCTTCCGGTTTCCCGGCTGGGCCGGAGCCCGACAGCGGC 120

Qy    121 AGCGCCGGCTCGGAGGACGGGCAGCGGCACGCGCCAGCGGCCGCGCACATCTCCCGGGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGCCGGCTCGGAGGACGGGCAGCGGCACGCGCCAGCGGCCGCGCACATCTCCCGGGGTC 180

Qy    181 ATCATCACGGCGGGTCTCACTCCGTAGTGTTCGTCGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGGTCTCACTCCGTAGTGTTCGTCGGCTTGGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300
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Db    241 ATGTTCGTGATCATCCGATACACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Db    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTCCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
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Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTCCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTCTTCATGAAGATCGGCTTCATCTTTGCCTTGCCTGTCGTCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCGGCTTCATCTTTGCCTTGCCTGTCGTCCTGTCCTC 720

Qy    721 ATCATCATGTCTGCTACACCCTGATGATCCTGGCTGTCCTCAAGAGCGTCCGGCTCCTTCT 780
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Db    721 ATCATCATGTCTGCTACACCCTGATGATCCTGGCTGTCCTCAAGAGCGTCCGGCTCCTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCGGTGGTGGTG 840

Qy    841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy    901 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCTCTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCTCTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCCTGCTTTCCACTGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTCCTGCTTTCCACTGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTTCAGGATCCTGCTTACCTGAGGGATGAATGAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTTCAGGATCCTGCTTACCTGAGGGATGAATGAAACCAGTA 1140

Qy   1141 TGA 1143
          |||
Db   1141 TGA 1143
```

RESULT 15
AAT12550
ID   AAT12550 standard; cDNA; 1142 BP.
XX
AC   AAT12550;
XX
DT   03-SEP-1996 (first entry)
XX
DE   Human kappa opioid receptor cDNA.
XX
KW   Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW   neurology; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1142
FT   /tag= a
FT   /product= "kappa opioid receptor"
FT   /note= "incomplete termination codon"
XX

```
PN   WO9601898-A1.
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995; 95WO-FR000912.
XX
PR   11-JUL-1994; 94FR-00008531.
XX
PA   (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX
PI   Kieffer B, Simonin F;
XX
DR   WPI; 1996-097628/10.
DR   P-PSDB; AAR88722.
XX
PT   New nucleic acid encoding the human Kappa opioid receptor - useful in
PT   diagnosis and therapy, and for isolating receptor ligands and modulators.
XX
PS   Claim 3; Page 13-15; 30pp; French.
XX
CC   This sequence codes for the human kappa opioid receptor and was obtained
CC   from two overlapping cDNA fragments isolated from a human placental cDNA
CC   library. The fragments were amplified from the library using PCR primers
CC   based on the sequence of human genomic clones which hybridised with a
CC   murine delta receptor cDNA probe. Nucleotide probes derived from the
CC   kappa opioid receptor coding sequence are useful for diagnosis of
CC   neurological, cardio- vascular and psychiatric disorders associated with
CC   opioid receptors
XX
SQ   Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;
```

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Query Match             98.8%;  Score 1140.4;  DB 2;  Length 1142;
Best Local Similarity   99.9%;  Pred. No. 6.1e-271;
Matches 1141;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
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Qy      1 ATGGGACTCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCCTACCTGGGCCCCGAGCGCC 60
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Db      1 ATGGGACTCCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCCTACCTGGGCCCCGAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGGCGGCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 AGCGCCGGCTCCGGAGGACGCGCAGCTGAGCCCGGCGACATCTCCCGGCCATCCCGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGCCGGCTCCGGAGGACGCGCAGCTGAGCCCGGCGACATCTCCCGCCCATCCCGGTC 180

Qy    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGTCGGCAACTCGCTGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGTCGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 CTGGCCTTTGGCAGATGCTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCCTTTGGCAGATGCTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCATCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCATCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTGCTCCTTGCCAGTTCCCAGATGATGACTACTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTGCTCCTTGCCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy    841 GCAGTCTTCGTCGTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTCGTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 900

Qy    901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Db    901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAAAACTTCAAGCGGGTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCTTGTCCACTGAAGATGAGGATGGAGGCGGCAGCACTAGCAGAGTC 1080
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Db   1021 TTCCGGGACTTCTGCTTCTTGTCCACTGAAGATGAGGATGGAGGCGGCAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TG 1142
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Db   1141 TG 1142
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        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April  6, 2005, 12:28:42 ; Search time 215 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%
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              5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
              6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match Match	Query Length	DB	ID	Description
1	1144.4	99.2	1182	4	US-09-016-434-1417	Sequence 1417, Ap
2	1141.4	98.9	1143	4	US-09-341-446B-1	Sequence 1, Appli
3	1140.4	98.8	1142	3	US-08-765-743-1	Sequence 1, Appli
4	1136.2	98.5	1284	4	US-09-341-446B-3	Sequence 3, Appli
5	1130.2	97.9	1143	4	US-09-826-509-542	Sequence 542, App
6	999.4	86.6	1275	4	US-09-341-446B-5	Sequence 5, Appli
7	994.6	86.2	1275	4	US-09-341-446B-7	Sequence 7, Appli
8	909.2	78.8	1408	4	US-09-214-904-5	Sequence 5, Appli
9	909.2	78.8	1410	3	US-08-147-592A-1	Sequence 1, Appli
10	909.2	78.8	1410	3	US-08-292-694A-1	Sequence 11, Appl
11	869.6	75.4	1000	3	US-08-147-592A-11	Sequence 11, Appl
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13	446.4	38.7	2135	4	US-08-430-286A-1	Sequence 1, Appli
14	444.8	38.5	1618	3	US-08-889-108-1	Sequence 1, Appli
15	444.8	38.5	1618	3	US-08-889-108-3	Sequence 3, Appli
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17	444.8	38.5	1618	3	US-08-120-601B-3	Sequence 3, Appli
18	444.8	38.5	1618	5	PCT-US94-10358-1	Sequence 1, Appli
19	444.8	38.5	1618	5	PCT-US94-10358-3	Sequence 3, Appli
20	434	37.6	1334	4	US-09-761-962A-1	Sequence 1, Appli
21	434	37.6	1365	4	US-09-761-962A-11	Sequence 11, Appl
22	434	37.6	1423	4	US-09-761-962A-1	Sequence 1, Appli
23	434	37.6	1610	4	US-09-761-962A-16	Sequence 16, Appl
24	434	37.6	1729	4	US-09-761-962A-9	Sequence 9, Appli
25	434	37.6	2045	4	US-09-761-962A-10	Sequence 10, Appl
26	433.2	37.5	1610	3	US-08-889-108-7	Sequence 7, Appli
27	433.2	37.5	1610	5	PCT-US94-10358-7	Sequence 7, Appli
28	433.2	37.5	2160	3	US-08-188-275A-1	Sequence 1, Appli
29	433.2	37.5	2162	3	US-09-351-198-1	Sequence 1, Appli
30	433.2	37.5	2162	4	US-09-113-426-1	Sequence 1, Appli
31	433.2	37.5	2162	4	US-09-016-434-1379	Sequence 1379, Ap
32	433.2	37.5	2162	4	US-09-355-709C-7	Sequence 7, Appli
33	432.4	37.5	2229	4	US-09-214-904-1	Sequence 1, Appli
34	430.8	37.3	1542	4	US-09-761-962A-4	Sequence 4, Appli
35	430.8	37.3	1981	3	US-08-387-707-15	Sequence 15, Appl
36	430.8	37.3	1981	4	US-08-405-271A-15	Sequence 15, Appl
37	430	37.3	1182	4	US-09-826-509-546	Sequence 546, App
38	430	37.3	1203	5	US-09-826-509-544	Sequence 544, App
39	422.6	36.6	1829	2	US-08-411-859-1	Sequence 1, Appli
40	422.6	36.6	1829	3	US-08-387-707-7	Sequence 7, Appli
41	422.6	36.6	1829	3	US-08-405-271A-7	Sequence 7, Appli
42	422.6	36.6	2218	4	US-09-214-904-3	Sequence 3, Appli
43	422.6	36.6	2219	4	US-08-432-174A-1	Sequence 1, Appli
44	422.6	36.6	2272	3	US-08-147-592A-3	Sequence 3, Appli
45	422.6	36.6	2272	3	US-08-292-694A-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-016-434-1417
; Sequence 1417, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;   APPLICANT: Janice Au-Young
;   APPLICANT: Jeffrey J. Seilhamer
;   TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
;   TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;   NUMBER OF SEQUENCES: 1490
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;     STREET: 3174 PORTER DRIVE
;     CITY: PALO ALTO
;     STATE: CALIFORNIA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/016,434
;     FILING DATE: HEREWITH
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Zeller, Karen J.
;     REGISTRATION NUMBER: 37,071
;     REFERENCE/DOCKET NUMBER: PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (650) 855-0555
;     TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1417:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1182 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: GENBANK
;       CLONE: g532059
US-09-016-434-1417                       Score 1144.4;  DB 4;  Length 1182;

  Query Match             99.2%;         Score 1144.4;
  Best Local Similarity   99.5%;         Pred. No. 1.8e-274;
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Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db  134 AGGCGCGGCTCGGAGGACGGCAGCTGGGACCCGCGCCACATCTCCCGCCATCCCGGTC 193

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db  194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy  241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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Db  314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

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Qy  661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCGTCTTCGTCATCCTGTCCTC 720
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Db  674 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCGTCTTCGTCATCCTGTCCTC 733

Qy  721 ATCATCATCGTCTGCTACACCCTGGTCTACACCCTGGTCTCTGATATCCTCCGGCTCCTTTCT 780
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Db  734 ATCATCATCGTCTGCTACACCCTGGTCTACACCCTGGTCTCTGATATCCTCCGGCTCCTTTCT 793

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCGAGACTGTCTCCTGGTGTGGTG 840
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Db  794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCGAGACTGTCTCCTGGTGTGGTG 853

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RESULT 2
US-09-341-446B-1
; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-341-446B-1

Query Match   98.9%; Score 1141.4; DB 4; Length 1143;
Best Local Similarity   99.9%; Pred. No. 9.9e-274;
Matches 1142; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   61 TGCCTGCCCCCAACAGCAGCGGCCGTCGGTTTCCCGGCTCGGCGCCCGACAGCAACGGC 120
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Db   61 TGCCTGCCCCCAACAGCAGCGGCCGTCGGTTTCCCGGCTCGGCGCCCGACAGCAACGGC 120

Qy  121 AGGCGCGGCTCGGAGGACGGCAGCTGGGACCCGCGCCACATCTCCCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGGCGCGGCTCGGAGGACGGCAGCTGGGACCCGCGCCACATCTCCCGGCCATCCCGGTC 180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db  301 CTGGCTTTGGCAGATGCTTTAGTTAGTTACTACAACCATGCCCTTTCAGAGTCGTCACTTG 360

Qy  361 ATGAATTCCTGGGATGTGCTGTGCAAGATAGTGTGCAAGATAGTAATTTCCATTGATTGATTACTAC 420
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Db  361 ATGAATTCCTGGGATGTGCTGTGCAAGATAGTGTGCAAGATAGTAATTTCCATTGATTGATTACTAC 420

Qy  421 AACATGTTCGTGATCTTCACCTTGACCATGATGAGCCGTCGGACCGCTACATTGCCGTC 480
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Db  421 AACATGTTCGTGATCTTCACCTTGACCATGATGAGCCGTCGGACCGCTACATTGCCGTC 480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
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Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGATGAATAAACCAGTA 1140
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;   APPLICATION NUMBER:   FR 94/08531
;   FILING DATE:   11-JUL-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:   WO PCT/FR95/00912
;   FILING DATE:   07-JUL-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:   PATCH, Andrew J
;   REGISTRATION NUMBER:   32,925
;   REFERENCE/DOCKET NUMBER:   NX 1758-1P US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:   (703) 521-2297
;   TELEFAX:   (703) 685-0573
;   TELEX:   248425 EMBON
INFORMATION FOR SEQ ID NO:   1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:   1142 base pairs
;   TYPE:   nucleic acid
;   STRANDEDNESS:   double
;   TOPOLOGY:   linear
;   MOLECULE TYPE:   cDNA
;   FEATURE:
;   NAME/KEY:   CDS
;   LOCATION:   1..1142
US-08-765-743-1

Query Match       98.8%;   Score 1140.4;   DB 3;   Length 1142;
Best Local Similarity   99.9%;   Pred. No. 1.8e-273;
Matches 1141;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300
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Db    241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300

Qy    301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCACTTG  360
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Db    301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCACTTG  360

Qy    361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGAGTAGTAATTTCCATTGATTACTAC  420
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Db    361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGAGTAGTAATTTCCATTGATTACTAC  420

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Qy    481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Db    481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy    541  TGCATCTGGCTGCTGTCGTCATCGTGTTGGCATCTCTGTTGCAATAGTCCTTGGAGGCACCAAA  600
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Db    541  TGCATCTGGCTGCTGTCGTCATCGTGTTGGCATCTCTGTTGCAATAGTCCTTGGAGGCACCAAA  600

Qy    601  GTCAGGGAAGACGTCGATGTCATTGAGTCGTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Db    601  GTCAGGGAAGACGTCGATGTCATTGAGTCGTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Qy    541  TGCATCTGGCTGCTGTCGTCATCTGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
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Qy    601  GTCAGGGAAGACGTCGATGTCATTGAGTCGTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Db    601  GTCAGGGAAGACGTCGATGTCATTGAGTCGTCCTTGCAGTTCCCAGATGATGACTACTCC  660

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Db    661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTCCGTGATCCCGTCCTC  720

Qy    721  ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
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Db    721  ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

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Qy    841  GCAGTCTTCGTTGTCTGCTGCGGACTCCCATTCACATATTCATCCTCGGTTGGAGGCTCTGGGG  900
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Qy    901  AGCACCTCCCACAGCACCAGCAGCTGCTCTCTCCCAGCTATTACTTCTGCATCCGCCTTAGGCTAT  960
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Db    901  AGCACCTCCCACAGCACCAGCAGCTGCTCTCTCCCAGCTATTACTTCTGCATCCGCCTTAGGCTAT  960

Qy    961  ACCAACAGTAGCCTGAATCCCATTCCTTCTACGCCTTTCTTTTGATGAAAACTTCAAGCCGGTGT  1020
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Db    961  ACCAACAGTAGCCTGAATCCCATTCCTTCTACGCCTTTCTTTTGATGAAAACTTCAAGCCGGTGT  1020

Qy   1021  TTCCGGACTTCTGCTTTCGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCACAGTC  1080
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Db   1021  TTCCGGACTTCTGCTTTCGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCACAGTC  1080

Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGGAATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGGAATGAATAAACCAGTA  1140

Qy   1141  TGA  1143
           |||
Db   1141  TGA  1143
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RESULT 3
US-08-765-743-1
;   Sequence 1, Application US/08765743
;   Patent No. 6146835
;   GENERAL INFORMATION:
;   APPLICANT:   KIEFFER, Brigitte
;   APPLICANT:   SIMONIN, Frederic
;   TITLE OF INVENTION:   HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC
;   TITLE OF INVENTION:   ACIDS AND USES THEREOF
;   NUMBER OF SEQUENCES:   6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:   YOUNG & THOMPSON
;   STREET:   745 South 23rd Street
;   CITY:   Arlington
;   STATE:   Virginia
;   COUNTRY:   U.S.A.
;   ZIP:   22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:   Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM:   PC-DOS/MS-DOS
;   SOFTWARE:   PatentIn Release #1.0,   Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:   US/08/765,743
;   FILING DATE:   11-FEB-1997
;   CLASSIFICATION:   536
;   PRIOR APPLICATION DATA:
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Qy  173  GCTGCCCCCAACAGCAGCGCCTCGGTTCCCGGCTGGGGCCGAGCCCGACAGCAGCAACGGCA  232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122  GCGCCGGCTCGGAGGACGCCGCAGCTGGAGCGCCGGCCGCACATCTCCCGGCCACATCCCGGTCA  181

Db  233  GGCCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCGGCCGCACATCTCCCGGCCACATCCCGGTCA  292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  182  TCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGGCAACTCGCTCGGTCA  241

Db  293  TCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGGCAACTCGCTCGGTCA  352

Qy  242  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAAACATTTACATATTAAACC  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  353  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAAACATTTACATATTAAACC  412

Qy  302  TGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGCTCACTTGA  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  413  TGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGCTCACTTGA  472

Qy  362  TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA  421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  473  TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA  532

Qy  422  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGACATTGCCGTGT  481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  533  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGACATTGCCGTGT  592

Qy  482  GCCACCCCGTGAGGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGTCATCAATATCT  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  593  GCCACCCCGTGAGGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGTCATCAATATCT  652

Qy  542  GCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTGTGGAGGCACCAAAG  601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  653  GCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTGTGGAGGCACCAAAG  712

Qy  602  TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  713  TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  772

Qy  662  GGTGGGGACCTCTTCATGAAGATCGGTCTTCATCTTTGCCTTCGTCTTGATCCCTGTCCTCA  721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  773  GGTGGGGACCTCTTCATGAAGATCGGTCTTCATCTTTGCCTTCGTCTTGATCCCTGTCCTCA  832

Qy  722  TCATCATCGTCTGCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTG  781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  833  TCATCATCGTCTGCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTG  892

Qy  782  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCCTGGTGGTGGTGG  841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  893  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCCTGGTGGTGGTGG  952

Qy  842  CAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTGGTGGATGCTGCCTTAGGCTATA  901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  953  CAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTGGTGGATGCTGCCTTAGGCTATA  1012

Qy  902  GCACCTCCCAGCACCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTGAAAACTTCAAGCGGTGTT  961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1013 GCACCTCCCAGCACCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTGAAAACTTCAAGCGGTGTT  1072

Qy  962  CCAAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTCTTGATGAAAACTTCAAGCGGTGTT  1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1073 CCAAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTCTTGATGAAAACTTCAAGCGGTGTT  1132

Qy  1022 TCCGGGACTTCTGCTTTCCACTGAGATGAGATGAGCGGCGGCACTAGCACTAGCAGAGTCC  1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1133 TCCGGGACTTCTGCTTTCCACTGAGATGAGATGAGCGGCGGCACTAGCACTAGCAGAGTCC  1192

Qy  1082 GAAATACAGTTCAGGATCCTGCTTACCTGACGCATGGGATGAATAAACCAGTAT  1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1193 GAAATACAGTTCAGGATCCTGCTTACCTGACGCATGGGATGAATAAACCAGTAG  1252

Qy  1142 G  1142
          |
Db  1253 G  1253
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RESULT 4
US-09-341-446B-3
; Sequence 3, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; APPLICANT: Conklin, Bruce R.
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
US-09-341-446B-3

Query Match   98.5%; Score 1136.2; DB 4; Length 1284;
Best Local Similarity 99.7%; Pred. No. 2e-272;
Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    2  TGGACTCCCCGATCCAGATCTTCCCGCGGGGAGCCCGGCGGGAGCCCTACCTGCCGCCCGAGCGCCT  61
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113  TCGACTCCCCGATCCAGATCTTCCCGCGGGGAGCCCGGCGGGAGCCCTACCTGCCGCCCGAGCGCCT  172

Qy   62  GCCTGCCCCCAACAGCAGCGCCTCGGTTCCCGGCTGGGGCCGAGCCCGACAGCAGCAACGGCA  121
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RESULT 5
US-09-826-509-542
; Sequence 542, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 542
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-542

Query Match   97.9%; Score 1130.2; DB 4; Length 1143;
Best Local Similarity 99.3%; Pred. No. 6e-271;
Matches 1135; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAATCCCCGATTCAGATCTTCCGGGGAGCCTGGCCCGCCCCTACCTGCGCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCGGCGGCTGGTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGGCGGCTGGTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 120

Qy   121 AGCGGCGGCTCGGAGGACGCGCCAGCTGGAGCCGCGGCCACATCTCCCGGCCATCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCGGCTCGGAGGACGCGCCAGCTGGAGCCGCGGCCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCGGCTTGGTGGGCAACTCGCTGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCGTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACATCCGTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCCGTCATCTGTTGGCATCCTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCGTCATCGTCATCTGTTGGCATCCTGCAATAGTCCTTGGAGGGCACCAAA 600

Qy   601 GTCAGGAAGACGTCGATGTCATTGAGTGCTCCTTGTCCAGTTCCCAGATGATGACTACTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGAAGACGTCGATGTCATTGAGTGCTCCTTGTCCAGTTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGGTCTTCATCTTTGCTCTCGTGATCCTCGTCCTC 720
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACACCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACACCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGAGGCTCTCGGGG 900
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGG 900

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGACGAGCGGCAGCAGACTAGCAGAGTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGACGAGCGGCAGCAGACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGA 1143
           |||
Db   1141 TGA 1143

RESULT 6
US-09-341-446B-5
; Sequence 5, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASSL OR1
US-09-341-446B-5

Query Match   86.6%; Score 999.4; DB 4; Length 1275;
Best Local Similarity 93.0%; Pred. No. 2e-238;
Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

Qy   2 TGGACTCCCGATCCAGATCTTCCGGGGAGCCGGGGGAGCCCTACCTGCGCCCCGAGCGCCT 61
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 TCGACTCCCCGATCCAGATCTTCCGGGGAGCCGGGGGAGCCCTACCTGCGCCCCGAGCGCCT 172

```
Qy    62 GCCTGCCCCAACAGCAGCGCCTGGTTTCCCGCTGGGCCGAGCCCGACAGCAACGGCA 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 GCCTGCCCCAACAGCAGCGCCTGGTTTCCCGCTGGGCCGAGCCCGACAGCAACGGCA 232

Qy   122 GGCCGGCTCGGAGGACGCGCCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTCA 181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 GGCCGGCTCGGAGGACGCGCCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTCA 292

Qy   182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGTGGCAACTCGCTGGTCA 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 TCATCACGGCGGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGTGGCAACTCGCTGGTCA 352

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTGA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTGA 472

Qy   362 TGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 TGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 532

Qy   422 ACATGTTCACCAGCATCTTCGACCATGATGAGCGTGGACCGCTACATTGCCGTGT 481
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   533 ACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGTTACATTGCCGTGT 592

Qy   482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCT 541
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   593 GCCACCCCGTGAAGGCTTTGGATTTCCGAACACCCTTTGAAAGCAAAGATCATCAACATCT 652

Qy   542 GCATCTGGCTGCTGTCGTCATCGTTGGCATCTGTGTTGGCAATAGTCCTTGGGGTGACCCAAC 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 GCATTTGGCTACTGGCCATCATCGTGTTGGTATATCAGCGGATAGTCCTTGGGGTGACCCAAC 712

Qy   602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCGAGTGACGACTACTCCT 661
         ||       ||||   || |||||||||||
Db   713 CCCGGGATGGAGGAGTAGTTGTATGCACGTCCACGCCC---------CAGTCTGGT 763

Qy   662 GGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTCA 721
         ||| ||   || |||||||||||||
Db   764 ACTGGGACACTGTGACCAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCA 823

Qy   722 TCATCATCGTCTACACACCCCTGCGTCTCAGAGGATCCTCAGAGAGCGTCCGGCTCCTTCTG 781
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   824 TCATCATCGTCTACACACCCCTGCGTCTCAGAGGATCCTCAGAGAGCGTCCGGCTCCTTCTG 883

Qy   782 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGGTGGTGGTGG 841
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   884 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGGTGGTGGTGG 943

Qy   842 CAGTCTTCGTTGTCTGCTGACTCCCATTCCAGCTGTCTCCGACTATCATCCTGGTGGAGGCTCTGGGGA 901
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   944 CAGTCTTCGTTGTCTGCTGTGGACTCCCATTCCAGCTGTCTCCGACTATCATCCTGGTGGAGGCTCTGGGGA 1003

Qy   902 GCACCCTCCCACAGCACGACAGCTGCTCCAGTCGCTCTTCTGCATGCTATTACTTCTGCGCCTTAGGCTATA 961
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1004 GCACCCTCCCACAGCACGACAGCTGCTCCAGTCGCTCTTCTGCATGCTATTACTTCTGCGCCTTAGGCTATA 1063

Qy   962 CCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCCGGTGTT 1021
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1064 CCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCCGGTGTT 1123

Qy  1022 TCCGGGACTTCTGTCTTTCACTGAAGATGAGCGGCGAGCGACTAGCAGAGTCC 1081
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1124 TCCGGGACTTCTGTCTTTCCACTGAAGATGAGCGGCGAGCGACTAGCAGAGTCC 1183

Qy  1082 GAAATACAGTTCAGGATCTCCAGGCACATCGATGGGGATGAATAAACCAGTAT 1141
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1184 GAAATACAGTTCAGGATCTCCAGGCACATCGATGGGGATGAATAAACCAGTAG 1243

Qy  1142 G 1142
         |
Db  1244 G 1244
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RESULT 7
US-09-341-446B-7
; Sequence 7, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RASSL OR2
US-09-341-446B-7

Query Match   86.2%; Score 994.6; DB 4; Length 1275;
Best Local Similarity   92.7%; Pred. No. 3e-237;
Matches 1058; Conservative   0; Mismatches 74; Indels   9; Gaps 1;

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Qy     2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCGAGCGCCT 61
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCGAGCGCCT 172

Qy    62 GCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCGCCGAGCAGCAACGGCA 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 GCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCGCCGAGCAGCAACGGCA 232

Qy   122 GCGCCGGCTCGGAGGACGCGCGCAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGTCA 181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 GCGCCGGCTCGGAGGACGCGCGCAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGTCA 292

Qy   182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGTGGCAACTCGCTGGTCA 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 TCATCACGGCGGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGTGGCAACTCGCTGGTCA 352

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGGTCA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TCATCACGCGGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGTGGCAACTCGCTGGTCA 472

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCGTCGGTCA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCGTCGGTCA 472

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGTGCTGTCAAGATAGTAATTACTACA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGTGCTGTCAAGATAGTAATTACTACA 472

Qy   242 TGTTCGTGATCATCCGATACACAAACAAAGATGAAGACAACAACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAACAAAGATGAAGACAACAACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGAGTACGGTCTACTTGA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGAGTACGGTCTACTTGA 472

Qy   242 TGTTCGTGATCATCCGATACAACAAAGATGAAGACAACACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACAACAAAGATGAAGACAACACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGAGTACGGTCTGGTCA 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGAGTACGGTCTGGTCA 472

Qy   242 TGTTCGTGATCATCCGATACAACACAAAGATGAAGACAACAACATTTACATATTTAACC 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACAACACAAAGATGAAGACAACAACATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTTGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGAATTCCTGGCCTTTTGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 532

Qy   422 ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTCGTGGACCGTTACATTGCCGTGT 481
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   533 ACATGTTTACCAGCATCATCACCTTGACCATGATGAGTGTGGACCGTTACATTGCCGTGT 592

Qy   482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCGAAGGCAAAGATCATCAATATCT 541
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   593 GCCACCCCGTGAAGGCTTTGGATTTCCGAACACCCTTGAAAGCAAAGATCATCAACATCT 652

Qy   542 GCATTGGCTGCTGTCGTCATCGTTGGCATCTGTGTTGGCAATAGTCCTTGGGGTGACCCAAC 601
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 GCATTTGGCTACTGGCCATCATCGTGTTGGTATATCAGCGGATAGTCCTTGGGGTGACCCAAC 712
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;           LOCATION:  184..1323
US-09-214-904-5

Query Match             78.8%;  Score 909.2;  DB 4;  Length 1408;
Best Local Similarity   86.7%;  Pred. No. 5.2e-216;
Matches 1001;           Conservative 0;  Mismatches 153;  Indels 0;  Gaps 0;

Qy       1 ATGGACTCCCGATCAGATCTTCCGCGGGAGCCGGGCCTACCTGCCGCCCGAGCGCC  60
           ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     184 ATGGAGTCCCCATTCAGATCTTCGATCCTGTGATCCCGTCCTGCTCTCCCAGTGCT 243

Qy      61 TGGCTGCCCCCACAGCAGCGCGCTGGTTCCCGCTGGTTCCCACTGGGCAGAATCCGA 120
           ||| |||||||||||||||||||| ||||||  |||||||| ||||||||||||||
Db     244 TGCCTTCTCTCCCCACAGCAGTCTCTGGTTCCCCAACTGGGCAGAATCCGACAGTAATGGC 303

Qy     121 AGCGGCCGGCTCGGAGGACGCGGCAGCTGAGCGTCCGGGCCACCATCTCCCCGGGCCATCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 AGTGTGGGCTCAGAGGATCAGCAGCAGCTGGAGTCCGGCGCACATCTCTCCGGCCATCCCGTGTT 363

Qy     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 ATCATCACCGCGTGTCTACCTCTGGTATTTGTCGTGACATTGGGCAATTCTCTGGTC 423

Qy     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCACCAACATTTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 ATGTTTGTCATCATCCGATACAACAGAAGATGAAGACCGCAACCAACATCTACATATTTAAC 483

Qy     301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 CTGGCTTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTCAGAGTGCGTCTACTTG 543

Qy     361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGGAAGATAGTAATTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 ATGAATTCTTGGCCTTTGTGGCCTTTGTGTATGCGAAGATTGTCATTCCATTGACTACTAC 603

Qy     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGGTGGACCGGTACACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGCTACACATTGCTGTG 663

Qy     481 TGCCACCCGTGAAAGCTTTGGACTTCCGCACACCCTTGAAAGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 TGCCACCCGTGAAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAGATCATCAACATC 723

Qy     541 TGCATCTGGCTGTCGTCATCTGTTGGCATCCTCGTTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||| | ||||||||||||||||||||||||||||||||||||||||||||
Db     724 TGCATTTGGCTCCTGGCATCATCGTTGTGTATCAGCGATAGTCCTTCGAGGCACCAAA 783

Qy     601 GTCAGGGAAGACGTTCGATGTCATTGAGTGCTTCCTTGCAGTTCCAGTGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 GTCAGGGAAGATGCTGGATGTCATTGGAATGCTCCTTGCAGTTCCTGATGAATGAATATTCC 843

Qy     661 TGGTGGGACCTCTTCATGAAGATCTCGGTCTTCATCTTCGCCTTCGTCGTGATCCCTGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 TGGTGGGATCTCTTCATGAAGAGATCGTGTCTTTGTCTTTGCCTTTGTGTGTCTGCCCAGTCCTC 903

Qy     721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 ATCATCATTGTCTGCTACACCCTGATGATCCTGCGTCTGCTAGGATCACCAGAGTGGTCTCGTGGTG 963

Qy     781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTCTAGAATCCTGGTCTGGTGCTGGTAGTAGTT 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     964 GGCTCCCGAGAGAGGAGGACCGGAAATCTCCGCGCATCACCAAGCTGGTGCTGGTAGTAGTT 1023

Qy     841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCACATCTTTATCCTGGTGGAGGGTCTCGGGG 900
           ||||||||||||||||||||||||||| | ||| ||||||||||||||||||||||||||
Db    1024 GCAGTCTTCATCATCTGTTGGACCCCCATTACCCATTCCACATCTTTATCCTGCTCGGGGA 1083

Qy     901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGTATTACTTCTGCATCGCCTTAGGCTAT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1084 AGCACCTCCCACAGCACCAGCTGCCTCTCCAGCTATTATTTCTTGTATTTCTGGTTAT 1143

Qy     961 ACCAACAGTAGCTGAATCCCATTTCTTCTACGCCGTTCTTCGGATGAAAACTTCAAGCAGTCGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
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(continued - second column)

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Qy     602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT 661
           ||||| |||||||||||||||||||||||||||||||||||||| -------||||||
Db     713 CCCGGGATGGAGCAGTGGTATGCACGGTCGTCTTCATCTTTGCCTTCATCTTCGTGATCCCTGTCCTCA 763

Qy     662 GGTGGGACCTCTTCATGAAGATCTGACCAAGATCGCGGTCTTCATCTTCGCCTTCATCTTCGTCCTCA 721
           ||||||  ||||||||||||||||||||||||||||||||||||| ||||||||
Db     764 ACTGGGACACTGTGACCAAGATCGCGTCTTCTTTGCCTTCATCTTCGTCCTCA 823

Qy     722 TCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCTTTCTG 781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     824 TCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCTTTCTG 883

Qy     782 GCTCCCGAGAGAAAGATCGCAACCTGCGGTAGGATCACCAGACTGGTCCTGGTGGTGGTGG 841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     884 GCTCCCGAGAGAAAGATCGCCAACCTGCGGTAGGATCACCAGACTGGTCCTGGTGGTGGTGG 943

Qy     842 CAGTCTTCGTTGTCTGGACTCCCATTCATCCTGGTGGAGGGCTCTGGGAG 901
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     944 CAGTCTTCGTCGTCTGGACTCCCATTCATCCTGGTGGAGGGCTCTGGGGGA 1003

Qy     902 GCACCTCCCACAGCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 961
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1004 GCACCTCCCACAGCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 1063

Qy     962 CCAACAGTAGCTGAATCCCATTCCTTCTACGCGCCTTTCTTGATGAAAACTTCAAGCGCGTGTT 1021
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1064 CCAACAGTAGCTGAATCCCATTCCTTCTACGCGCCTTTCTTGATGAAAACTTCAAGCGCGTGTT 1123

Qy    1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTCC 1081
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGCAGAGCACTAGCAGAGTCC 1183

Qy    1082 GAAATACAGTTCAGGATCCGGGATCCTGCTTACCTGAGCGGACATCGAGCGACATCGAGGGGGACATCGAGGGGGACATCGAGAATAAACCAGTAT 1141
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1184 GAAATACAGTTCAGGATCCTGCTTACCTGAGCGGACATCGAGGGGGACATGGGATGGAATGAATAAACCAGTAG 1243

Qy    1142 G 1142
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Db    1244 G 1244
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RESULT 8
US-09-214-904-5
; Sequence 5, Application US/09214904
; Patent No. 6632977
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
;   TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
;   NUMBER OF SEQUENCES: 6
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/214,904
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/FR97/01282
;   FILING DATE:
;   APPLICATION NUMBER: FR 96.08810
;   FILING DATE: 15-JUL-1996
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1408 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS

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Qy      1  ATGGACTCCCGATCCAGATCTTCCGGCGGAGCGCGGGCCTTACCTGCGCCCCGAGCGCC     60
           ||||||| ||| || |||||||||||||||||| | ||| || ||||||||||  | ||
Db    186  ATGGAGTCCCCATTCAGATCTTCCGGCGGAGATCCAGGCCCTACCTGCGCTCCCAGTGCT    245

Qy     61  TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCTGGCGAGCCCGAGCAGCAACGGC     120
           ||||| || |||||||||| | ||||||||| ||||| |||| ||||| |||  ||||
Db    246  TGCCTTCTCCCAACAGCAGCTCTGGTTCCCCAACTGGGCAGCAGAATCCCGACAGTAATGGC 305

Qy    121  AGGCCCGGCTCGGAGGACGCGGCAGCTGGAGCGGCCGCCACATCTCCCGGCCATCCCGGTC  180
           || | ||||||||||||| | || |||| || |||||||||||||||| ||||||||| ||
Db    306  AGTGTGGGCTCAGAGGATCAGCAGCTGAGTCCGGCCGCCACATCTCCGGCCATCCCTGTT    365

Qy    181  ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCGTTGGTGGGCAACTCGCTGGTC 240
           |||||||| | | || ||||| || |||| ||| ||| || || ||||||||| |||||||
Db    366  ATCATCACCGTGTCTACTCTGTCGTGTATTGTTGTGTGGTGGTGGGCGTTAGTGGGCAATTCTCTGGTC 425

Qy    241  ATGTTCGTGATCATCCGATCACAAAGATGAAGACAGCAACATTACACATTTACATATTTAAC 300
           ||||| ||| || || |||| |||||||||| || | ||||| ||| ||||||||| |||
Db    426  ATGTTTGTCATCATCCGATCACCGATCACCGAGAGATGAAGACCGCAACCAACATCTACATATTTAAC 485

Qy    301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTG    360
           |||||||| ||||||||||| ||| ||||||| |||||||| |||| || ||| ||||||
Db    486  CTGGCTTTGGCAGATGCTTTGGTTACTACCACATGCCCTTTCAGATGCGTGTCTACTTG    545

Qy    361  ATGAATTCCTGGCCTTTTGGGGATGTCGTGTCAAGATAGTAATTCCATTGATTACTAC    420
           ||||||| |||| ||||||| ||||| ||| | | |||| || ||||||||||| |||||
Db    546  ATGAATTCTTGGCCTTTTGGAGATGTCTATGCCATGCAAGATTGTCATTTCCATTGACTACTAC 605

Qy    421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG  480
           || ||||||||| || |||||||| ||||| |||||| || || || ||||| ||| |||
Db    606  AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCCGCTACATTGCTGTG  665

Qy    481  TGCCACCCCTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC   540
           ||||| || ||||||||||||||| ||| ||||| |||||||||||||||| |||| |||
Db    666  TGCCACCCTGAAGGCTTTGGACTTCCGGAACCACCTTTGAAAGCAAAGATCATCAACATC   725

Qy    541  TGCATCTGGCTGCTGTCTTCTGGCATCGTGTTGGCATCTGCAATAGTGTCTTGATCAGCAGGATACTAC 600
           ||||||||||| | ||| ||||| ||||| ||| ||||| |||| || |||||| ||||| ||||||||
Db    726  TGCATTTGGCCTGCTGTCTTCTGGGATATCAGGATATCATGGTATATCAGGATACTAC   785

Qy    601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC   660
           ||||||||||| || || |||||| || || ||| | |||||||||| ||||| ||||||
Db    786  GTCAGGGAAGAGATGTGGATGTCATTGAGTGTCATTGCAGTTTCTGATGATGAATATTCC   845

Qy    661  TGGTGGGACCTCCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCTCTGCTTGCCTC   720
           |||||| ||| | ||||||||||| ||| ||| ||||| ||| ||| |||| |||| |||
Db    846  TGGTGGGATCTCTTCATGAAGATCGTGTCTTGTCTTTGCCTTTTGTGATCCCAGTCCTC   905

Qy    721  ATCATCATGTCTGCTACACCCTGATGATCCTGCCGTCTCAAGAGAGGTCCGGCTCCTTCT   780
           ||||||||||| ||| ||| ||||||| || || ||| |||||||| |||| || |||||
Db    906  ATCATCATTGTCTGCTACACCCTGATGATCCTGCCGCCTGAAGAGTGTCCGCCTCCTGTCT   965

Qy    781  GGCTCCCGAGAGAAAGATGCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG   840
           |||| ||| |||||| |||| ||| || |||||||||||||| |||||||| |||||||
Db    966  GGCTCCCGAGAGAAGAAGACCGAAATCTCCGCGCCATCACCAAGCTGGTGTGGTAGTAGTT  1025

Qy    841  GCAGTTCGTGTTGTCTGCTGACTCCAATATTCATCCTGGTGTGAGGCTCTGGGG   900
           |||||| ||||| ||||||||| |||||| || |||| |||| | ||| |||||
Db   1026  GCAGTCTTCATCATCGTTGTTGACCCCCATTCATCTTTATCCTGTGGAGGCTCTGGGGA  1085

Qy    901  AGCAACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCGATCGCCTTAGGCTAT  960
           ||||| ||||||||| |||||||||| || |||||| || ||||| | || ||||||||||
Db   1086  AGCACCTCCCACAGCACAGCTGCCCTCTCCAGCTATTATTTCTGTATTATTTCTGGGTTAT 1145

Qy    961  ACCAACAGTAGCCTGAATCCTGGTCTCTTCTTCTTAGCCCTTTCTTCTAGAAAACTTCAAGCCGGTGT 1020
           || |||||| || |||||||| ||||| |||| |||  |||| |||||||||||||||| |||||||
Db   1146  ACCAACAGCAGCCTGAATCCTGTTCTTTTCTTCTAGCCTTTATTTCTTGATGAAAACTTCAAGCCGGTGT 1205

Qy   1021  TTCCGGGACTTCTGCTTTGCTTCCACTGAAGATGAAGATGAGGATGAGGAGCGCCAGAGTC 1080
           |||||  ||||||| ||| ||||| || |||||||||||||| |||||||| ||||| |||
Db   1206  TTTAGGGACTTCTGTCTTCCCTATTAAGATGCGAATGGAGCGCCAGAGCACCAATAGAGTT 1265

Qy   1081  CGAAATACAGTTCAGGATCCTGCTACCTGAGGGACATCGATGGGATGAATAAACCAGTA   1140
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(left-hand continuation block)

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Db   1144  ACCAACAGCAGCCTGAATCCTGTTCTCTATGCCTTTCTGGATGAAAACTTCAAGCGGTGT 1203
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Qy   1021  TTCCGGGACTTCTGCTTTGCTTCCACTGAAGATGAAGATGAGGATGAGGAGCGCCAGAGTC 1080
           ||  ||||||||| ||| |||||| || || || |||| |||| |||||| ||||| ||||
Db   1204  TTTAGGGACTTCTGTCTTCCCTATTAAGATGCGAATGGAGCGCCAGAGCACCAATAGAGTT 1263

Qy   1081  CGAAATACAGTTCAGGATCCTGCTACCTGAGGGACATCGATGGGATGAATAAACCAGTA   1140
           ||||| ||||||||||||||||||  ||| ||||| |  ||||||| ||| || |||||
Db   1264  AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGGAGGGATGAATAAGCCAGTA 1323

Qy   1141  TGACTAGTCGTGGA 1154
           ||||||||||||||
Db   1324  TGACTAGTCGTGGA 1337
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RESULT 9
US-08-147-592A-1
; Sequence 1, Application US/08147592A
; Patent No. 6096513
GENERAL INFORMATION:
;   APPLICANT: Bell, Graeme I
;   APPLICANT: Reisine, Terry
;   APPLICANT: Yasuda, Kazuki
;   TITLE OF INVENTION: Opioid Receptor Genes,
;   TITLE OF INVENTION: Compositions and Methods
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 72210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/147,592A
;   FILING DATE: 05-NOV-1993
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30-JUL-1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20-MAY-1993
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:105
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1410 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 186..1325
US-08-147-592A-1

Query Match   78.8%; Score 909.2; DB 3; Length 1410;
Best Local Similarity   86.7%; Pred. No. 5.2e-216;
Matches 1001; Conservative   0; Mismatches 153; Indels   0; Gaps   0;

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RESULT 10
US-08-292-694A-1
; Sequence 1, Application US/08292694A
; Patent No. 6319686
; GENERAL INFORMATION:
;   APPLICANT: BELL, GRAEME
;   APPLICANT: REISINE, TERRY
;   APPLICANT: YASUDA, KAZUKI
;   TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
;   NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Arnold, White & Durkee
;     STREET: P. O. Box 4433
;     CITY: Houston
;     STATE: Texas
;     COUNTRY: USA
;     ZIP: 77210
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/292,694A
;     FILING DATE: August 19, 1994
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/066,296
;     FILING DATE: 20 May 1993
;     CLASSIFICATION: 435
;     APPLICATION NUMBER: 08/100,694
;     FILING DATE: 30 July, 1993
;     CLASSIFICATION: 435
;     APPLICATION NUMBER: 08/147,592
;     FILING DATE: 5 No. 6319686ember 1993
;     CLASSIFICATION: 435
;     APPLICATION NUMBER: PCT/US94/05747
;     FILING DATE: 20 May 1994
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MARK B. WILSON
;     REGISTRATION NUMBER: 37,259
;     REFERENCE/DOCKET NUMBER: ARCD:140/WIM
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (512) 418-3000
;     TELEFAX: (713) 789-2679
;     TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1410 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: genomic DNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 186..1325
US-08-292-694A-1

Query Match  78.8%;  Score 909.2;  DB 3;  Length 1410;
Best Local Similarity  86.7%;  Pred. No. 5.2e-216;
Matches 1001;  Conservative 0;  Mismatches 153;  Indels 0;  Gaps 0;

Qy    1 ATGGACTCCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
         || || ||||| |||| ||||||||||| ||  ||||| ||  ||||| || || ||||||
Db  186 ATGGAGTCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCCAGTGCT 245

Qy   61 TGGCTGCCCCCAACAGCAGCGGCTGGTTTCCCGGTCTGGGCCGAGCCCCGACAGCAACGGC 120
         |||| ||||||||||||||||| | || ||||  || ||||| |||||||| ||| ||||
Db  246 TGGCCTTCTCCCAACAGCAGCGACGCTCTTGGTTCCCAACTGGCAGAATCCGACAGTAATGGC 305

Qy  121 AGCGCCGGCTCGGAGGACGCGGCCAGCTGAGTCGAGCTGGAGTCCGGCCACATCCCCGGTC 180
         || ||||| ||||||||||| |||||||  |   ||  |||||||||||||||||||||||
Db  306 AGTGTGGGGTCAGAGGATCAGACAGCAGCTGGAGTCCGGCCACATCTCCGGCCATCCCCTGTT 365

Qy  181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGAGTGTTGGTGGGCAACTCGCTGGTC 240
         ||||||||  | ||| || ||  || ||||| ||  ||||||||||||| | | ||||||
Db  366 ATCATCACCGCTGTCTACTCTGTGGTATTTGTGTGGGCTTAGTGGGCAATTCTCTGGTC 425

Qy  241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCACCACACATTTACATATTTAAC 300
         ||||| ||||||||||||||| | ||||||||| || || || |||||||||||||||
Db  426 ATGTTTGTCATCATCCGATACACGAAGATGAAGACCGAACCAACATCTACATATTTAAC 485

Qy  301 CTGGCTTTGGCAGATGCTTAGTTACTACAACAATGCCCTTCAGAGTACGGTCTACTTG 360
         ||||||||||||||||||| || ||||| || | |||||||||||| || || | ||||
Db  486 CTGGCTTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTCAGAGTGCGTCTGTCACTTG 545

Qy  361 ATGAATTCCTGGGCCTTTTGGGGATGTGCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
         |||||||| ||||||||||||| |||||||  | |||||||| |  || ||||||| |||||||
Db  546 ATGAATTCTTGGGCCTTTTGGGAGATGTGCTATGCAAGATTGTCATTTCCATTGACTACTAC 605

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATGCCCGTG 480
         ||||||||| |||||||| |||||||||||||||||| ||||||||||||||| || |||
Db  606 AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGCTACATTGCTGTG 665

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
         |||||||||||||| |||||||||||||| |||||| ||||| |||||||||||| ||||
Db  666 TGCCACCCCGTGAAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAGATCATCAACATC 725

Qy  541 TGTATCTGGCTGCTGTCGTCATCGTTGGCATCTGTGAGATCCTTGGAGGCACCAAA 600
         || |||||||| || ||||| ||||||| ||| |  ||| ||||||||||||||||
Db  726 TGCATTTGGCTCCTGGCATCATCGTTGTATATCAGCGATAGTCCTTGGAGGCACCAAA 785

Qy  601 GTCAGGGAAGACGCTGGATGTCATTGAGTGTCCTCCCAGCAGTTCCCAGATGACTACTCC 660
         |||||||||||  |||||||||||||||||  || || |  || ||  |||| ||||||||
Db  786 GTCAGGGAAGATGGGATGTCATTGAGTGATGCGCTACGTTTCCTGATGATGAATATTCC 845

Qy  661 TGGTGGGACCTCTTCATGAAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
         ||||||| ||||||||||||| ||||| ||||  || ||||||| ||||||||  |||||
Db  846 TGGTGGGGATCTTCTTCATGAAGATCGTGTTCTTGCCTTTGTGATCCCCAGTCCTC 905

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         |||||||| ||||||||||||||||||||||||| ||| |||||| ||||| ||||| ||
Db  906 ATCATCATTGTCTGCTACACCCTGATGATCCTGCGCCTGCGAAGAGTGTCCGAGCTCCTGTCT 965

Qy  781 GGCTCCCGAGGAAAGATCGCAACCTGCGCTAGGATCACCAGACTGCCTGGTGTGGTGGTG 840
         |||||||||| ||| || | || ||||| |  || |||  |  ||  | || ||||||  |
Db  966 GGCTCCCGAGAGAAGGACCGAAATCTCCGCCGACGAAATCTCCGGTGGTGGTGGTAGTT 1025

Qy  841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATCTTTATCCTGGTGAGGCTCTGGGGG 900
         ||||||||| | ||| ||  |||||||||||| ||| |||| ||||||||||||||  ||||||||||
Db 1026 GCAGTCTTCATCATCGTTGGACCCCATTCCATTCACATCTTTATCCTGGTGGAGGCTCTGGGGA 1085

Qy  901 AGCACCTCCCACAGCACAGCTGCTCTTCTCCAGTATTACTTCTGCATGCCTTAGGCTAT 960
         |||||||||||||||||||||||  ||||||||||| | ||||| || | ||| ||||
Db 1086 AGCACCTCCCACAGCACAGCTGCCCTCTCCAGTATTATTTTCTGTATATTCTGGTTAT 1145

Qy  961 ACCAACAGTAGCCAGAATCCCATTCTCCACTGAAGATGAGGATGCAGCGGCAGCACTAGCAGAGTC 1020
         |||||||| ||||| |||| | ||||| | | ||||||||| ||  | | || ||  | |||  |
Db 1146 ACCAACAGCAGCCAGGAAATCCTGTTCTCTCTCATGCCTTTCTGTGATGAAAACTTCAAGCGGTGT 1205

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGCGGAGCGGCACTAGCACAGAGTC 1080
         || | ||||||||||||| |  |  |||| |  ||| | |||| || ||| ||||||||
Db 1206 TTTAGGGACTTCTGCTTCCCTATTAAGATGGAATGGAAGTGGAGCGCCAGAGCCACCAATAGAGTT 1265

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGGACATCGATGGGGACATCGATGGGAATAAACCAGTA 1140
         ||||| |||||||||||||||||||| |||| | | ||| | || |  ||| | |||||| |||||
Db 1266 AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGAGTGGGAGGGATGAATAAGCCAGTA 1325

Qy 1141 TGACTAGTCGTGGA 1154
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Db 1326 TGACTAGTCGTGGA 1339
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Qy   1141 TGACTAGTCGTGGA 1154
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Db   1326 TGACTAGTCGTGGA 1339

RESULT 11
US-08-147-592A-11
; Sequence 11, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
;   APPLICANT: Bell, Graeme I
;   APPLICANT: Reisine, Terry
;   APPLICANT: Yasuda, Kazuki
;   TITLE OF INVENTION: Opioid Receptor Genes,
;   TITLE OF INVENTION: Compositions and Methods
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 72210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/147,592A
;   FILING DATE: 05-NOV-1993
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30-JUL-1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20-MAY-1993
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:105
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;   NAME/KEY: N
;   LOCATION: 607-608, 642-643, 895, 906
;   IDENTIFICATION METHOD: N = A, C, G or T
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 102..986
;   FEATURE:
;   NAME/KEY: Xaa
;   LOCATION: 169, 181, 265, 269
;   IDENTIFICATION METHOD: Xaa = unknown
US-08-147-592A-11

Query Match   75.4%; Score 869.6; DB 3; Length 1000;
Best Local Similarity 97.5%; Pred. No. 3.1e-206;
Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

Qy   244 TTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG 303
Db   87 TTCTTTTCTTTTAGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG 146
                        ||||||||||||||||||||||||||||||||||||||||||||||

Qy   304 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 206

Qy   364 AATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTACAAC 423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 AATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTACAAC 266

Qy   424 ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTCACATTGCCGTGTGC 483
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   267 ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGC 326

Qy   484 CACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC 543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327 CACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC 386

Qy   544 ATCTGGCTGCTGTCGTCCATCTGTTGGCATCCTGCAATAGTCCTTGGAGGCACCAAAGTC 603
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   387 ATCTGGCTGCTGTCGTCGTCCATCTGTTGGCATCCTGCAATAGTCCTTGGAGGCACCAAAGTC 446

Qy   604 AGGAAGACGTCGATGTCATTGAGTGAGTGCTGCTCCCAGATGATGACTACTTCCTGG 663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   447 AGGAAGGTGTCGATGTCATTGAGTGAGTGCTGCTGCTCCCAGATGATGACTACTTCCTGG 506

Qy   664 TGGGACCTCTTCATGAGAGATCGCGTCTTCATCTTGCCTTCGTGATCCCGTCCTCATC 723
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   507 TGGGACCTCTTCATGAGAGATCGCGTCTTCATCTTGCCTTCGTGATCCCGTCCTCATC 566

Qy   724 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGC 783
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   567 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGANNGTCCGGCTCCTTTCTGGC 626

Qy   784 TCCCGAGAAAGATCGCAACCTGGTAGGATCACCAGACTGGTCCTGGTGGTGGCA 843
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   627 TCCCGAGAAAGAGATNNCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCA 686

Qy   844 GTCTTCGTTGCTCGCTGGACTCCCATTCACATATCATCCTCGGTGGAGGCTCGGGGAGC 903
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   687 GTCTTCGTCGTCGCTGGACTCCCATTCACATATCATCCTCGGTGGAGGCTCGGGGAGC 746

Qy   904 ACCTCCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACC 963
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   747 ACCTCCCACACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACC 806

Qy   964 AACAGTAGCCTGAATCCCATTCTTCCTGATGAAAACTTCAAGCGGGTGTTTC 1023
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   807 AACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTTGATGAAAACTTCAAGCGGGTGTTTC 866

Qy   1024 CGGGACTTCGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCAGAGTCCGA 1083
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   867 CGGGACTTCGCTTTCCACTGAAGATGAGAATGGGACGCGCNAGAGCACTAGCAGAGTCCGA 926

Qy   1084 AATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATG---GATGAATAAACCAGTA 1140
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   927 AATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATGATGAATAAACCAGTA 986

Qy   1141 TGACTAGTCGTGGA 1154
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Db   987 TGACTAGTCGTGGA 1000

RESULT 12
US-08-292-694A-11
; Sequence 11, Application US/08292694A
; Patent No. 6319686
; GENERAL INFORMATION:
;   APPLICANT: BELL, GRAEME
;   APPLICANT: REISINE, TERRY
;   APPLICANT: YASUDA, KAZUKI
;   TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

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Qy   424  ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGC  483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   267  ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGC  326

Qy   484  CACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC  543
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327  CACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC  386

Qy   544  ATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC  603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   387  ATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC  446

Qy   604  AGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTCCCAGTGCTGCCGTCCTCCTG  663
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   447  AGGGAAGTGTCGATGTCATTGAGTGCTCCTTGCAGTCCCAGTGCTGCCGTCCTCCTG  506

Qy   664  TGGGACCTTCTCATGAAGATCTGGTCTTCATCTTGCCTTCGTCGTGATCCTCCTCATC  723
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   507  TGGGACCTTCTCATGAAGATCTGCTCTTCATCTTGCCTTCGTCGTGATCCCTGTCCTCATC  566

Qy   724  ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCTCGGC  783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   567  ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCTCGGC  626

Qy   784  TCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCA  843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   627  TCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCA  686

Qy   844  GTCTTCGTTGTCTGCTGGACTCCATTCATCCTGGGAGGCTCTGGGGAGC  903
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   687  GTCTTCGTTGTCTGCTGGACTCCATTCATCCTGGGAGGCTCTGGGGAGC  746

Qy   904  ACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCGTTCTGCATCGCCTTAGGCTATACC  963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   747  ACCCCCACAGCACAGCTGCTCTCTCCAGCTATTCGTTCTGCATCGCCTTAGGCTATACC  806

Qy   964  AACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAATGAAACTTCAAGCGGTGTTC  1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   807  AACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAAACTTCAAGCGGTGTTTC  866

Qy   1024 CGGGACTTCTGCTTCCACTGAAGATGAGGCGGCAGAGTCAGAGTCCGA  1083
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   867  CGGGACTTCTGCTTCCACTGAAGATGAGNATGGAGCGCNAGAGCCAGAGTCCGA  926

Qy   1084 AATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGG---GATGAATAAACCAGTA  1140
          ||||||||||||||||||||||||||||||||||||||||   |||||||||||||||||
Db   927  AATACAGTTCAGGATCCTGCTTACCTGAGGGAGGATGGGGATGAATGAATAAACCAGTA  986

Qy   1141 TGACTAGTCGTGGA  1154
          ||||||||||||||
Db   987  TGACTAGTCGTGGA  1000
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RESULT 13
US-08-430-286A-1
; Sequence 1, Application US/08430286A
; Patent No. 6225080
; GENERAL INFORMATION:
;   APPLICANT: Uhl, George R.
;   APPLICANT: Eppler, C. Mark
;   APPLICANT: Wang, Jai-Bel
;   TITLE OF INVENTION: Mu-Subtype Opioid Receptor
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Darby & Darby PC
;   STREET: 805 Third Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: US
;   ZIP: 10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

; NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/292,694A
;   FILING DATE: August 19, 1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20 May 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30 July, 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/147,592
;   FILING DATE: 5 No. 6319686ember 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: PCT/US94/05747
;   FILING DATE: 20 May 1994
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MARK B. WILSON
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:140/WIM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (713) 789-2679
;   TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: N
;   LOCATION: 607-608, 642-643, 896, 906
;   IDENTIFICATION METHOD: N = A, C, G or T
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 102..986
;   FEATURE:
;   NAME/KEY: Xaa
;   LOCATION: 169, 181, 265, 269
;   IDENTIFICATION METHOD: Xaa = unknown
US-08-292-694A-11

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Query Match    75.4%;   Score 869.6;  DB 3;   Length 1000;
Best Local Similarity 97.5%;  Pred. No. 3.1e-206;
Matches  891;  Conservative   0;  Mismatches  20;  Indels   3;  Gaps   1;

Qy   244  TTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG  303
          ||||                  |||||||||||||||||||||||||||||||||||||||
Db   87   TTCTTTTCTTTTAGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG  146

Qy   304  GCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCACTTGATG  363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147  GCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCACTTGATG  206

Qy   364  AATTCCTGGCCTTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC  423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207  AATTCCTGGCCTTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC  266
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COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/430,286A
FILING DATE:  28-APR-1995
CLASSIFICATION:  536
ATTORNEY/AGENT INFORMATION:
NAME:  Robinson, Joseph R.
REGISTRATION NUMBER:  33,448
REFERENCE/DOCKET NUMBER:  0646/1A843-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE:  212-527-7700
TELEFAX:  212-753-6237
TELEX:  236687
INFORMATION FOR SEQ ID NO:  1:
SEQUENCE CHARACTERISTICS:
LENGTH:  2135 base pairs
TYPE:  nucleic acid
STRANDEDNESS:  single
TOPOLOGY:  linear
MOLECULE TYPE:  cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM:  Rattus rattus
IMMEDIATE SOURCE:
CLONE:  mu receptor cDNA
US-08-430-286A-1
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Query Match      38.7%;    Score 446.4;  DB 3;   Length 2135;
Best Local Similarity  66.9%;    Pred. No. 5.7e-101;
Matches    668;   Conservative    0;  Mismatches  321;  Indels    9;  Gaps    2;

Qy   110 ACAGACAACGGCAGCCGCCGGCTCGGAGGACGGCGCAGCTGGAGCCCCGCGCACATCTCCCCCG  169
         ||||||||||| || |||||||| ||||| || || | |||||| || ||||||||||||| |||
Db   167 ACCGCACCGGGCTTGGCGGGGAACAGACAGCCTGTGCCCTCAGACCGGCAGCCCTTCCATGG  226

Qy   170 CCATCCCGGTCATCATCACGCGGTCTACTCCGTAGTGTTCGTCTGTGGCTTGGTGGGCA  229
         |||| |||| ||| | ||||||| |||| ||| ||| |||| || |||| |
Db   227 TCACAGCCATTACCATCATGGCCCTCTATCTCTACTCTGTGTGTAGTGTGTGGGCCTCTTCGGAA  286

Qy   230 ACTCGCTGGTCATGTTCGTGATCATCCGATCACAAAGATGAAGACAGCAACCAACATTT  289
         |||| | |||| |||||||| ||||| |||| |||||||||||| | | |||||||||||
Db   287 ACTTCCTGGTCATGTATGTGATTGTAAGATACACCAAAAATGAAGACTGCCACCAACATCT  346

Qy   290 ACATATTAACCTGGCTTTGGCAGAGTGCTTTAGTTACTACACAACCATGCCCTTCAGAGTA  349
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Db   347 ACATTTTCAACCTGCTCTGGCAGACGCCTTAGCGACCAGTACACTGCCCTTTCAGAGTG  406

Qy   350 CGGTCTACTTGATGAATTCCTGGCCTTTGGGGATGCGTGTCAAGATAGTAATTTCCA  409
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Db   407 TCAACTACCTGATGGGAACATGGCCCTTCGGAACATCCTCGAACATCGCAAGATCGTGATCTCAA  466

Qy   410 TTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCT  469
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Db   467 TAGATTACTACAACATGTTCACCAGCATATTCACCCTGCACCATGAGCGTGGACCGCT  526

Qy   470 ACATTGCCGTGCCACCCCGTGAAGGCTTTGGACTTCCCGCACACCCTTGAAGGCAAAGA  529
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Db   527 ACATTGCTGTGCGCCACCAGTCAAAGCCCTGGATTTCCGTACCCCCCGAAATGCCAAAA  586

Qy   530 TCATCAATATCTGGCTCGTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTG  589
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Db   587 TCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCATCGGTCTGCCTGTAATGTTCATGG  646

Qy   590 GAGGCACCAAAGTCAGGGAAGACGTCGATGTGCATTGAGTGCTCCAGTTCCCAGATG  649
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Db   647 CAACCACAAAATACAGGCAGGGGTC------CATAGATTGCACCCCTGCTTCTTCCACC  700

Qy   650 ATGACTACTCCGTGTGGGACCCTCTCATGATGAAGATCTGCGTCTTCATCCTTTGCCTTCGTGA  709
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Db   701 CAACCTGGTACTGGGAAATACAGGCAGGGGTCTGCTC---AAAATCTGTGTCTTTATCTTCGCTTTCATCA  757

Qy   710 TCCCTGTCCTCATCATCACCGTCTGCTACACCCTGATGATCCTGCGTCTGCTCAAGAGAGCGTCC  769
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RESULT 14
US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;   APPLICANT: Yu, Lei
;   TITLE OF INVENTION: Mu Opioid Receptors: Compostions and Methods
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/889,108
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/305,518
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: INDA005\WIM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1618 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (cDNA)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 214..1410
;
US-08-889-108-1

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Db   758 TGCCGGTCCTCATCATCACTGTGTTACGGCCTGATGATCTTACGACTCAAGAGCGTTC  817
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Qy   770 GGCTCCTTCTGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCC  829
             |||||| ||| ||||| |||||||| |||||| ||| |  || ||| |||||||||
Db   818 GCATGCTATCGGCTCCAAAGAAGAAGGACAGACAGGAATCTGCGCAGGATCACCCGATGGTGC  877
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RESULT 15
US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;   APPLICANT: Yu, Lei
;   TITLE OF INVENTION: Mu Opioid Receptors: Compostions and Methods
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/889,108
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/305,518
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: INDA005\WIM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1618 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (cDNA)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 339..1235
;
US-08-889-108-3

Query Match   38.5%; Score 444.8; DB 3; Length 1618;
Best Local Similarity 66.8%; Pred. No. 1.3e-100;
Matches 667; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

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Qy   170 CCATCCCGGTCATCATCACGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCA 229
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Db   410 TCACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTGTAGTGGGCCTCTTCGGAA 469

Qy   230 ACTCGCTGGTCATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTT 289
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Db   470 ACTTCCTGGTCATGTATGTGATTGTAAGATACACCAAAATGAAGACTGCCACCAACATCT 529

Qy   290 ACATATTTAACCTGGCTTGGCAGCAGATGCTTAGTTACTACAACACATGGCCCTTTCAGAGTA 349
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Db   770 TCGTCAACGTCTGCAACTGGATCCTCTCCTCCGCCATCGGTCTGCCTGTAATGTTCATGG 829

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Db   830 CAACCACAAAATACAGGCAGGGGTC------CATAGATTGCACCCCCAGCGTTCTCCCACC 883

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Qy   770 GGCTCCTTTTGCTCCCGGCTCCCAAAGAAAGAAAGTCGCAACCTGCGTAGGGATCACCCGATCC 829
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Qy   830 TGGTGGTGGGTGGCAGTTCGTTGCTGCTGTATTTATCGTCTGCGACACAGCTGTTCATCCTCGGTGG 889
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Db  1061 TGGTGGTCGGTGGCACCTCCACATCGGACTCTCCAGCTATTACTTCTGCATCG 949

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Db  1181 CTTTGGGTGTTACACGAACAGCTGCTGCTGCTTCTTCTTTACGGCTCTTGCTGGATGAGAGAACT 1240

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Db   650  TAGATTACTACAACACATGTTCACCAGCACATATTCACCCTCTGCACCATGAGCGTGGACCGCT 709

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Db  1241  TCAAGCGATGCTTCAGAGAGTTCTTGCATCCCAACCTCGTCCACGATCGAACAGCAAAACT 1300

Qy  1070  CTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTAC 1107
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Search completed: April 6, 2005, 12:39:38
Job time : 218 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: April 6, 2005, 12:28:42 ; Search time 766.333 Seconds
(without alignments)
9125.590 Million cell updates/sec

Title: US-09-904-584-2
Perfect score: 1154
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Gapop 10.0 , Gapext 1.0
Searched: 5615251 seqs, 3030001701 residues
Total number of hits satisfying chosen parameters: 11230502
Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1154	100.0	1154	11	US-09-904-584-2	Sequence 2, Appli
2	1152.4	99.9	1154	11	US-09-904-584-1	Sequence 1, Appli
3	1152.4	99.9	1602	19	US-10-278-698-45	Sequence 45, Appl
4	1152.4	99.9	1602	19	US-10-278-698-559	Sequence 559, App
5	1150.8	99.7	1154	11	US-09-904-584-3	Sequence 3, Appli
6	1150.8	99.7	1154	11	US-09-904-584-4	Sequence 4, Appli
7	1150.8	99.7	1154	11	US-09-904-584-5	Sequence 5, Appli
8	1150.8	99.7	1154	11	US-09-904-584-6	Sequence 6, Appli
9	1150.8	99.7	1154	11	US-09-904-584-7	Sequence 7, Appli
10	1144.4	99.2	1182	15	US-10-225-567A-147	Sequence 147, App
11	1144.4	99.2	1182	15	US-10-345-680-19	Sequence 19, Appl
12	1144.4	99.2	1182	17	US-10-305-720-1417	Sequence 1417, Ap
13	1144.4	99.2	1182	18	US-10-283-975A-80	Sequence 80, Appl
14	1141.4	98.9	1143	16	US-10-318-661-1	Sequence 1, Appli
15	1136.2	98.5	1284	16	US-10-318-661-3	Sequence 3, Appli
16	1133.4	98.2	1143	15	US-10-345-680-21	Sequence 21, Appl
17	1130.2	97.9	1143	19	US-09-826-509-542	Sequence 542, App
18	1130.2	97.9	1143	19	US-10-925-095-542	Sequence 542, App
19	999.4	86.6	1275	16	US-10-318-661-5	Sequence 5, Appli
20	994.6	86.2	1275	16	US-10-318-661-7	Sequence 7, Appli
21	979.4	84.9	1875	16	US-10-318-661-13	Sequence 13, Appl
22	963.4	83.5	1875	16	US-10-318-661-15	Sequence 15, Appl
23	909.2	78.8	1408	9	US-09-214-904-5	Sequence 5, Appli
24	877.8	76.1	1911	16	US-10-318-661-17	Sequence 17, Appl
c 25	469	40.6	585	13	US-10-027-632-188121	Sequence 188121,
c 26	469	40.6	585	13	US-10-027-632-188122	Sequence 188122,
c 27	469	40.6	585	17	US-10-027-632-188121	Sequence 188121,
c 28	469	40.6	585	17	US-10-027-632-188122	Sequence 188122,
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30	444.8	38.5	1618	10	US-09-841-720-3	Sequence 3, Appli
31	434.6	37.7	1464	14	US-10-185-083-25	Sequence 25, Appl
32	434.2	37.6	2951	14	US-10-185-083-21	Sequence 21, Appl
33	434	37.6	1332	14	US-10-185-083-22	Sequence 22, Appl
34	434	37.6	1334	9	US-09-761-962-3	Sequence 3, Appli
35	434	37.6	1334	15	US-10-283-300-3	Sequence 3, Appli
36	434	37.6	1365	9	US-09-761-962-11	Sequence 11, Appl
37	434	37.6	1365	15	US-10-283-300-11	Sequence 11, Appl
38	434	37.6	1373	14	US-10-185-083-51	Sequence 51, Appl
39	434	37.6	1423	9	US-09-761-962-1	Sequence 1, Appli
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41	434	37.6	1440	14	US-10-185-083-15	Sequence 15, Appl
42	434	37.6	1569	14	US-10-185-083-17	Sequence 17, Appl
43	434	37.6	1610	9	US-09-761-962-16	Sequence 16, Appl
44	434	37.6	1610	15	US-10-283-300-16	Sequence 16, Appl
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ALIGNMENTS

RESULT 1
US-09-904-584-2
; Sequence 2, Application US/09904584
; Publication No. US2004009704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

Query Match 100.0%; Score 1154; DB 11; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60

Qy   61 TGGCTGCCCCCCAACAGCAGCAGCGGCTGGTTTCCCGGCGTCGGCGCCCGAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
US-09-904-584-1

; Sequence 1, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-1

  Query Match   99.9%; Score 1152.4; DB 11; Length 1154;
  Best Local Similarity   99.9%; Pred. No. 0;
  Matches 1153; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCCGCCGACAGCACGGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCCGCCGACAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGACGGGCCCGGCCACATCTCCCGGCCATCCCGGTC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGACGGGCCCGGCCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGACATCTTCACCTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGACATCTTCACCTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCGTCATCTGG... CAATAGTCCTTGGAGGCACCAAA 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCGTCATCTGGTCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTTCCCAGTTCCCAGATGATGACTACTCC 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTTCCCAGTTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCCTTCGTGATCCCTGTCCCTC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTGCCTTCGTGATCCCTGTCCCTC 720

Qy   721 ATCATCGTCTGCTACACCCCTGGAGATCCTGCGTCTTCAAGAGCGTCCGGCTCCTTTCT 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCGTCTGCTACACCCCTGGAGATCCTGCGTCTTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGGTAGGATCCACCAGACTGGTCCTGGTGGTGGTG 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGGTAGGATCCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTTGTCTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTTGTCTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCACAGCACAGCACAGCTGAATCCGCTATTACTTCTGCATCGCCTTAGGCTAT 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCACAGCACAGCTGAATCCGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCATTCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCATTCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGGACTTCGTTTCTGCTTTGCTTTCCACTGAAGATGAGGATGAGCGGCACTAGCAGAGTC 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGGACTTCGTTTCTGCTTTGCTTTCCACTGAAGATGAGGATGAGCGGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCGCTTACCTGAGGGCATCGATGGGATGAATAAACCAGTA 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCGCTTACCTGAGGGCATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
             ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGTTCGTCGTGTGGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGTTCGTCGTGTGGGTGGGCAACTCGCTGGTC 615

Qy   241 ATGTTGTGATCATCCGATACACAAAGATGAAGACAGCAGAA||||GAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   616 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGAACAGCAGAACCAACATTTACATATTTAAC 675

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 735

Qy   361 ATGAATTCCTGGCCTTTGGGGATGGTGTCTTGTCGTGAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   736 ATGAATTCCTGGCCTTTGGGGATGGTGTCTTGTCGTGAAGATAGTAATTTCCATTGATTACTAC 795

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATGTCGCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   796 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATGTCGCGTG 855

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   856 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 915

Qy   541 TGCATCTGGCTCGTCGTCATCTGTTGGCATCTCGTCAGTCTCCCAGTCGATGACTACTCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   916 TGCATCTGGCTCGTCGTCATCTGTTGGCATCTCGTCAGTCTCCCAGTCGATGACTACTCC 975

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTCCTTGCCTTCATCTTTGCCTTCGTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   976 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTCCTTGCCTTCATCTTTGCCTTCGTCC 1035

Qy   661 TGGTGGGACCTCTTCATGAAGATCTCGTCTTCAGAGCGTCCGGCTCCTTCT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 TGGTGGGACCTCTTCATGAAGATCTCGTCTTCAGAGCGTCCGGCTCCTTCT 1095

Qy   721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 1155

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGATCACCAGCACTGTCGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGATCACCAGCACTGTCGGTG 1215

Qy   841 GCAGTCTTCGTTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCAGTCTTCGTTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 1275

Qy   901 AGCACCTCCACAGCCTGAATCCCATTCTCTACGCGCCTTTGATGAAACTTCAAGCGGTGT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AGCACCTCCACAGCCTGAATCCCATTCTCTACGCGCCTTTGATGAAACTTCAAGCGGTAT 1335

Qy   961 ACCAACAGTAGCCTGAAATGGGGATGAATGGGATGAATAAACCAGTA 1020
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 ACCAACAGTAGCCTGAAATGGGGATGAATGGGATGAATAAACCAGTA 1395

Qy   1021 TTCCGGGACTTCGTGCTTTCCACTGAAGATGAGGATGAGGCGGCACTGAGGTT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 TTCCGGGACTTCGTGCTTTCCACTGAAGATGAGGATGAGGCGGCACTGAGGTT 1455

Qy   1081 CGAAATACAGTTCAGGATCTCGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CGAAATACAGTTCAGGATCTCGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1515

Qy   1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db   1516 TGACTAGTCGTGGA 1529

RESULT 4
US-10-278-698-559
; Sequence 559, Application US/10278698

Qy   661 TGGTGGGACCTCTTCATGAAGATCTCGCGTCTTCATCTTTGCCTTCGTGATCCTGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTCGCGTCTTCATCTTTGCCTTCGTGATCCTGTCCTC 720

Qy   721 ATCATCGTCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCGTCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGATCACCAGCACTGTCGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTGGATCACCAGCACTGTCGGTG 840

Qy   841 GCAGTCTTGTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTGTGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCACAGCCAGCAGCTGAATCCCATTCTCTACGCGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCCAGCAGCTGAATCCCATTCTCTACGCGCCTTAGGCTAT 960

Qy   961 AGCACCTCCCAGCACAGCCAGCAGCTGCTCTCTCTGGTTTCGCTTACCTGCCTTAGGCTAT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AGCACCTCCCAGCACAGCCAGCAGCTGCTCTCTCTGGTTTCGCTTACCTGCCTTAGGCTAT 1020

Qy   1021 TTCCGGGACTTCGTGTCTGCTTACCTGAGATGAGGATGAGGCGGCACTGAGAGTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCGTGTCTGCTTACCTGAGATGAGGATGAGGCGGCACTGAGAGTC 1140

Qy   1081 CGAAATACAGTTCAGGATCTTCCGCGGAGCCGGGAGCCCGAGCGCC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCTTCCGCGGAGCCGGGAGCCCGAGCGCC 1140

Qy   1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154

RESULT 3
US-10-278-698-45
; Sequence 45, Application US/10278698
; Publication No. US2005003734A1
; GENERAL INFORMATION:
;   APPLICANT: PathoArray GmbH
;   APPLICANT: Stuhlmuller, Bruno
;   APPLICANT: Haupl, Thomas
;   TITLE OF INVENTION: Nucleic Acid Array
;   FILE REFERENCE: O30027US
;   CURRENT APPLICATION NUMBER: US/10/278,698
;   CURRENT FILING DATE: 2002-10-23
;   NUMBER OF SEQ ID NOS: 1050
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1602
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-278-698-45

Query Match   99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy   1   ATGGACTACCCCGATCCAGATCTTCCGCGGGAGCCGGGAGCCCTACCTGCGCCCCGAGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 ATGGACTACCCCGATCCAGATCTTCCGCGGGAGCCGGGAGCCCTACCTGCGCCCCGAGCGCC 435

Qy   61   TGCCTGCCCCCAACAGCAGCGCGCCTGCGTTCCCGGCTCGGGCGGCCGGAGCCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 TGCCTGCCCCCAACAGCAGCGCGCCTGGCGTTCCCGGCTCGGGCGGCCGGAGCCCGACAGCAACGGC 495

Qy   121 AGCGCCCGGCTCGGAGGACGCGCAGCTGACGCTCCGGCCCGCGACATCCCCGGCCATCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 AGCGCCCGGCTCGGAGGACGCGCAGCTGACGCTCCGGCCCGCGACATCCCCGGCCATCCCGGTC 555

; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-559

Query Match   99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1153; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCCTACCTGCGCCCCGAGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCCTACCTGCGCCCCGAGCGCC 435

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 495

Qy   121 AGGCGCGGCTCGGAGGACGCGCAGCTGGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 AGGCGCGGCTCGGAGGACGCGCAGCTGGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTC 555

Qy   181 ATCATCACGGCGGGTCACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 ATCATCACGGCGGGTCACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 615

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 675

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGTCCCTTTCAGATGACTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGTCCCTTTCAGATGACTACGGTCTACTTG 735

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   736 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 795

Qy   421 AACATGTTCACCAGACATCTTCACCTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   796 AACATGTTCACCAGACATCTTCACCTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 855

Qy   481 TGCCACCCCGTGAAGGCTTGGACTTCCGACAGCAAAGATCATCAATATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   856 TGCCACCCCGTGAAGGCTTGGACTTCCGACAGCAAAGATCATCAATATC 915

Qy   541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGAGGCACCAAA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   916 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGAGGCACCAAA 975

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   976 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 1035

Qy   661 TGGTGGGACCTCTTCATGAAGATCGCCTTTGCCTTCGTTCATCTTTGTCCTGTCCTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 TGGTGGGACCTCTTCATGAAGATCGCCTTTGCCTTCGTTCATCTTTGTCCTGTCCTC 1095

Qy   721 ATCATCACGGCGGGTCACTCCGTAGTGTTCGTGTGGCTTGGTGGGCAACTCGCTGGTC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 ATCATCACGGCGGGTCTCACACCCTGATGATCCCTGCGTCTCAAGAGACGTCCGGCTCCTTTCT 1155

RESULT 5
US-09-904-584-3
; Sequence 3, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-3

Query Match   99.7%; Score 1150.8; DB 11; Length 1154;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1152; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCCTACCTGCGCCCCGAGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCCGATCCCGATCCAGATCTTCCGCGGGAGGCCCTACCTGCGCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120

Qy   121 AGCGCCCGGCTCGGAGGACGCGGAGGACGCTGGAGGACGCGGAGCCGCCACATCTCCCGGCCATCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCCGGCTCGGAGGACGCGGAGGACGCTGGAGGACGCGGAGCCGCCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGCGGTCACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGCGGTCACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGTGGTGGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGTGGTGGTG 1215

Qy   841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCATCCTCGTGTGGAGGCTCTGGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCATCCTCGTGTGGAGGCTCTGGGG 1275

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1335

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCAGCCTTTCTTGATGAAAACTTCAAGCGCGGTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 ACCAACAGTAGCCTGAATCCCATTCCAGCCTTTCTTGATGAAAACTTCAAGCGCGGTGT 1395

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGGAGATGGAGCGGCGAGCACTAGCAGAGTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGGAGATGGAGCGGCGAGCACTAGCAGAGTC 1455

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTAACCTGGAGGACATCGATGGGATGGAATAAACCAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CGAAATACAGTTCAGGATCCTGCTTAACCTGGAGGACATCGATGGGATGGAATAAACCAGTA 1515

Qy   1141 TGACTAGTCGTGGA 1154
              ||||||||||||||
Db   1516 TGACTAGTCGTGGA 1529

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; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 4
;  LENGTH: 1154
;  TYPE: DNA
;  ORGANISM: homo sapiens
US-09-904-584-4

Query Match             99.7%;     Score 1150.8;    DB 11;  Length 1154;
Best Local Similarity   99.8%;     Pred. No. 0;
Matches 1152;   Conservative    0;   Mismatches    0;  Indels    2;   Gaps    0;

Qy     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCGGGCCTACCTGCCCCCGAGCGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCGGGCCTACCTGCCCCCGAGCGCGCC 60

Qy    61 TGCCTGCCCCCAACAGCAGCGGCCCGCGACGCTGGAGCTGGGCGAGCCCACGCAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGGCCCGCGACGCTGGAGCTGGGCGAGCCCACGCAGCAACGGC 120

Qy   121 AGGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTACATTGCCGTG 480

Qy   481 TGGCACCCCGTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||
Db   481 TGGCACCCCGTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACCTGCATGCTCATTGAGTCTCCTTGCCGTG 660
           |||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACCTGCATGCTCATTGAGTCTCCTTGCCGTG 660

Qy   661 TGGTGGGACCTTCTGCTTCATGAAGATCTGCGTCTTCGTCCCTC 720
           ||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTTCTGCTTCATGAAGATCTGCGTCTTCGTCCCTC 720

Qy   721 ATCATCATCGTCGTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCGTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAAAGATGCGAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCGTCAAGCCGGTGT 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCGTCAAGCCGGTGT 480

Qy   481 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCACTAGCAGAGTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCACTAGCAGAGTC 540

Qy   541 CGAAATACAGTTCAGGATCCTGCTTACCTGACATCCTGGCATCTCTGTCGTCATCTGTTGGA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGAAATACAGTTCAGGATCCTGCTTACCTGACATCCTGGCATCTCTGTCGTCATCTGTTGGA 600

Qy  1141 TGACTAGTCGTCGGA 1154
           |||||||||||||||
Db  1141 TGACTAGTCGTCGGA 1154

RESULT 6
US-09-904-584-4
; Sequence 4, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
```

```
Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTCGGTGTGGTGTG  840

Qy      841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGTGGAGGCTCTGGGG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGTGGAGGCTCTGGGG  900

Qy      901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy      961 ACCAACAGTAGCCTGAATCCCATTCTCACGCGCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACAGTAGCCTGAATCCCATTCTCACGCGCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1020

Qy     1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy     1141 TGACTAGTCGTGGA  1154
            ||||||||||||||
Db     1141 TGACTAGTCGTGGA  1154
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RESULT 7
US-09-904-584-5
; Sequence 5, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-5

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  Query Match             99.7%;  Score 1150.8;  DB 11;  Length 1154;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1152  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy        1 ATGGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCGCCTACCTGCGCCGCCGAGCGCGCC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCGCCTACCTGCGCCGCCGAGCGCGCC  60

Qy       61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC  120

Qy      121 AGCGCCGGCTCGGAGGACGCGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCGCCGGCTCGGAGGACGCGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC  180

Qy      181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC  240

Qy      241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTAAC  300
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Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTAAC  300

Qy      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCACTTG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCACTTG  360

Qy      361 ATGAATTCCTGGCCTTTGGGATGCGTGTGCAAGATAGTAATTCCATTGATTACTAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATGAATTCCTGGCCTTTGGGATGCGTGTGCAAGATAGTAATTCCATTGATTACTAC  420

Qy      421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG  480

Qy      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy      541 TGCATCTGGCTGCTCGTCATCTGTTGGCATCTCGCAATAGTCCTTGGAGTGCACCAAA  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGCATCTGGCTGCTCGTCATCTGTTGGCATCTCGCAATAGTCCTTGGAGTGCACCAAA  600

Qy      601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy      661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGCCTTCGTGTCCTC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGCCTTCGTGTCCTC  720

Qy      721 ATCATCATGTCTGCTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ATCATCATGTCTGCTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGTG  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGTG  840

Qy      841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGTGGAGGCTCTGGGG  900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGTGGAGGCTCTGGGG  900

Qy      901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy      961 ACCAACAGTAGCCTGAATCCCATTCTCTTCTTGATGAAAACTTCAAGCGCGTGT  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACAGTAGCCTGAATCCCATTCTCTTCTTGATGAAAACTTCAAGCGCGTGT  1020

Qy     1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy     1141 TGACTAGTCGTGGA  1154
            ||||||||||||
Db     1141 TGACTAGTCGTGGA  1154
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RESULT 8
US-09-904-584-6
; Sequence 6, Application US/09905584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid

```
;  TITLE OF INVENTION:  Receptor Gene, Diagnostic Methods Using Said Allelles, and
;  TITLE OF INVENTION:  Methods of Treatment Based Thereon
;  FILE REFERENCE: 600-1-285N
;  CURRENT APPLICATION NUMBER: US/09/904,584
;  CURRENT FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: 60/218,300
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 6
;  LENGTH: 1154
;  TYPE: DNA
;  ORGANISM: homo sapiens
US-09-904-584-6

Query Match        99.7%;    Score 1150.8;    DB 11;    Length 1154;
Best Local Similarity  99.8%;    Pred. No. 0;
Matches 1152;    Conservative    0;    Mismatches    2;    Indels    0;    Gaps    0;

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGAGCCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGAGCCCGACAGCAACGGC 120

Qy     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy     181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy     301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy     361 ATGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy     421 AACAGTGTTCACCAGCATCTTCACCCTGACCATGAGCGTGGACCGCTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACAGTGTTCACCAGCATCTTCACCCTGACCATGAGCGTGGACCGCTACATTGCCGTG 480

Qy     481 TGCCACCCCGTGAAGGCTTTGGAGGCTTTGGACTTCCGCAATCTCTTGAGGCACCAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGCCACCCCGTGAAGGCTTTGGAGGCTTTGGACTTCCGCAATCTCTTGAGGCACCAAA 540

Qy     541 TGCATCTGGCTCGTGCTCGTCATCTGGCTCATCGTGCTCCTTGCCAGTTCCCGAGATGACTACTCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCATCTGGCTCGTGCTCGTCATCTGGCTCATCGTGCTCCTTGCCAGTTCCCGAGATGACTACTCC 600

Qy     601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy     661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGTCCGTTCGTGATCCCGTCCTC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGTCCGTTCGTGATCCCGTCCTC 720

Qy     721 ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCCGGCTCCTTTCT 780

Qy     781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCCAGACTGGTCCTGGTGGTGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCCAGACTGGTCCTGGTGGTGGTG 840

Qy     841 GCAGTCTTCGTGTCGTCTGGACTCCCATTCACATATTCACATATTCTCCGGTGGAGGCTCTCGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GCGGTCTTCGTGTCGTCTGGACTCCCATTCACATATTCACATATTCTCCGGTGGAGGCTCTCGGGG 900

Qy     901 AGACCTCCCACAGCACAGCACAGCTGCTTCTGTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AGACCTCCCACAGCACAGCACAGCTGCTTCTGTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960

Qy     961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTCTCTACGCCTTCTGATGAAAACTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTCTCTACGCCTTCTGATGAAAACTTCAAGCGGTGT 1020

Qy    1021 TTCCGGACTTCTGCTTTCCACTGAAGATGAGACGGCGCAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGACGGCGCAGAGCACTAGCAGAGTC 1080

Qy    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy    1141 TGACTAGTCGTGA 1154
           |||||||||||||
Db    1141 TGACTAGTCGTGA 1154


RESULT 9
US-09-904-584-7
;  Sequence 7, Application US/09904584
;  Publication No. US20040097704A1
;  GENERAL INFORMATION:
;  APPLICANT:  Kreek, Mary Jeanne
;  APPLICANT:  Yuferov, Vadim
;  APPLICANT:  LaForge, Karl Steven
;  TITLE OF INVENTION:  Alleles of the Human Kappa Opioid
;  TITLE OF INVENTION:  Receptor Gene, Diagnostic Methods Using Said Allelles, and
;  TITLE OF INVENTION:  Methods of Treatment Based Thereon
;  FILE REFERENCE: 600-1-285N
;  CURRENT APPLICATION NUMBER: US/09/904,584
;  CURRENT FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: 60/218,300
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 7
;  LENGTH: 1154
;  TYPE: DNA
;  ORGANISM: homo sapiens
US-09-904-584-7

Query Match        99.7%;    Score 1150.8;    DB 11;    Length 1154;
Best Local Similarity  99.8%;    Pred. No. 0;
Matches 1152;    Conservative    0;    Mismatches    2;    Indels    0;    Gaps    0;

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGAGCCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGAGCCCGACAGCAACGGC 120

Qy     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy     181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy     301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy     361 ATGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy     421 AACAGTGTTCACCAGCATCTTCACCCTGACCATGAGCGTGGACCGCTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACAGTGTTCACCAGCATCTTCACCCTGACCATGAGCGTGGACCGCTACATTGCCGTG 480

Qy     481 TGCCACCCCGTGAAGGCTTTGGAGGCAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGCCACCCCGTGAAGGCTTTGGAGGCAAGGCAAAGATCATCAATATC 540

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGAGCCTGGAGCCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGAGCCTGGAGCCCGACAGCAACGGC 120

Qy     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy     181 ATCATCACGGGCGTCTACTCCGTCGTCCGTCGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGGCGTCTACTCCGTCGTCCGTCGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAGCAGCAACCAACATTTACATATTAAC 300
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;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:     2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 147
;  LENGTH: 1182
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-225-567A-147

Query Match             99.2%;  Score 1144.4;  DB 15;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1148;  Conservative    0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCCGCC 60
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Db     14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCCGCC 73

Qy     61 TGCCTGCCCCAAACAGCAGCGCCTGGTTTCCCGGCGTGGGCGAGCGCCGAGCAGCAACGGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 TGCCTGCCCCAAACAGCAGCGCCTGGTTTCCCGGCGTGGGCGAGCGCCGACGAGCAACGGC 133

Qy    121 AGGGCCGGCTCGGAGGACAGCGGCAGCTGGAGCCCGGCACATCTCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AGGGCCGGCTCGGAGGACAGCGGCAGCTGGAGCCCGGCACATCTCCCGGCCATCCCGGTC 193

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCGGCTTGGTGGGCAACTCGCTGGTC 253

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 313

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy    361 ATGAATTCCTGGCCTTTGGGGATGGCGTGCTGCGAAGATGTAATTTCCAATGATTACTAC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ATGAATTCCTGGCCTTTGGGGATGGCGTGCTGCGAAGATGTAATTTCCAATGATTACTAC 433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 493

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTCATCTGTGGCAATAGTCCTTCTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTGGCTGCTGTCGTCATCGTCATCTGTGGCAATAGTCCTTCTGGAGGCACCAAA 613

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCAGTTCCCAGATGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCAGTTCCCAGATGATGACTACTCC 673

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTGCCTTCGTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTGCCTTCGTGTCCTC 733

Qy    721 ATCATCATCTGCTACACCCTGATGATCCTGCGCTCTCAAGAGAGTTCGGCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 ATCATCATCTGCTACACCCTGATGATCCTGCGCTCTCAAGAGAGTTCGGCTCCTTTCT 793

Qy    781 GGCTCCCGAGAGAAAGATCGGCAACCTGCTAGGATCACCAGACTGTCCTGGTGGTCGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCCGAGAGAAAGATCGGCAACCTGCTAGGATCACCAGACTGTCCTGGTGGTCGGTG 853
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Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||                ||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCATCTGTGGATCTTCTGCAATAGTCCTTGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTCATCTGTGGATCTTCTGCAATAGTCCTTGAGGCACCAAA 600

Qy    601 GTCGGGGAAGACGTCGATGTCATTGAGTGCTCCCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCGGGGAAGACGTCGATGTCATTGAGTGCTCCCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTCTTGCCTTCATCTTTGCCTTTGTCTTCGTGATCCTGTGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTTCTTGCCTTCATCTTTGCCTTTGTCTTCGTGATCCTGTGTCCTC 720

Qy    721 ATCATCATCTGCTACACCCTGATGATCCGGCTCTCAAGAGCGTCCGGCTCCGGCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCTGCTACACCCTGATGATCCGGCTCTCAAGAGCGTCCGGCTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAAAGATCGCAACCTGGTCTCCGGTGGTGGGG 840
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Db    781 GGCTCCCGAGAAAGATCGCAACCTGGTCTCCGGTGGTGGGG 840

Qy    841 GCAGTTTCGTCGTCGTGCTCGGGG 900
          ||||||||||||||||||||||||
Db    841 GCAGTTTCGTCGTCGTGCTCGGGG 900

Qy    901 AGCACCTCCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGGCGGCAGAGCACTAGCAGAGTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGAATAAAACCAGTA 1140
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Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGGAATAAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
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Db   1141 TGACTAGTCGTGGA 1154
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RESULT 10
US-10-225-567A-147
; Sequence 147, Application US/10225567A
; Publication No. US2003011379BA1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCGGGCCCTACCTGCGCCGCCCGAGCGCC  60
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Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCGGCCTCGGCCTACCTGCGCCCCGAGCGCC  73

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCTGGCCGACAGCAGCAACGC  120
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Db   74 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCTGGCCGACAGCAGCAACGC  133

Qy  121 AGGCCGGCTCGGAGGACGGCGCAGCTGAGCGACTGAGCGCACATCTCCCGGCCATCCGGTC  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 AGCGCGGCTCGGAGGACGGCGCAGCTGAGCGACGACTGAGCGCACATCTCCCGGCCATCCGGTC  193

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTCGTCGTGGCTGCGTGGGTTGTGTGGGCAACTCGCTGGTC  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  194 ATCATCACGGCGGTCTACTCCGTAGTGTCGTCGTGGCTGCGTGGGTTGTGTGGGCAACTCGCTGGTC  253

Qy  241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGACAGCAACCAACATTACATATTATTAAC  300
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Db  254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTATTAAC  313

Qy  301 CTGGCTTTGGCAGATGCTTGTTAGTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
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Db  314 CTGGCTTTGGCAGATGCTTGTTAGTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  373

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTGCTGCTGGCTGCGTGCAAGATAGTAATTCCATTGATTACTAC  420
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Db  374 ATGAATTCCTGGCCTTTGGGGATGTGCTGCTGGCTGCGTGCAAGATAGTAATTCCATTGATTACTAC  433

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGACCATTGCCGTG  480
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Db  434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGACCATTGCCGTG  493

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
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Qy  541 TGCATCTGGCTGCGTCGTCATCGTTGGCATCTGTTGGCATCTGCAATAGTCCTTGGAGGCACCAAA  600
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Db  554 TGCATCTGGCTGCGTCGTCATCGTTGGCATCTGTTGGCATCTGCAATAGTCCTTGGAGGCACCAAA  613

Qy  601 GTCAGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  614 GTCAGGGAGGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  673

Qy  661 TGGTGGGACCTTCATGAAGATCTGCCTTCGTCATCTTCGTGCTTCATCTTTGCCTTCCTC  720
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Db  674 TGGTGGGACCTTCATGAAGATCTGCCTTCGTCATCTTTGCCTTCGTCATCTTTGCCTTCCTC  733

Qy  721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGACACCTGCGAACCTGCGAACCTGGTC  780
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Db  734 ATCATCATCGTCTGCTACACACCCTGATGATCCTGACACCTGCGAACCTGCGAACCTGGTC  793

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCATCCTGGTCCTGGTGGTG  840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  794 GGCTCCCGAGAGAGAAGATCGCAACCTGCGCAGGATCACCAGATCATCCTGGTGGAGGTCCTGGTGGTG  853

Qy  841 GCAGTCTTCGTTGTCGTGTGTCTGCTGGACTCCCATTCACATATTCATCCTGCTATTACTTCTGCATCGCCTTAGGCTAT  900
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Db  854 GCGGTTTTCGTTGTCGTGTGTCTGCTGGACTCCCATTCCACATATTCATCCTGCTATTACTTCTGCATCGCCTTAGGCTAT  913

Qy  901 AGCACCTCCACAGCACAGCACAGCTCTCTCTCTCTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT  960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  914 AGCACCTCCACAGCACAGCACAGCTCTCTCTCTCTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT  973

Qy  961 ACCAACAGTAGCCTGAATCCGATCCCATTCCTCTACGCCTTTCTGATGAAAAACTTCAAGCGGTGT  1020
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Db  974 ACCAACAGTAGCCTGAATCCGATCCCATTCCTCTACGCCTTTCTGATGAAAAACTTCAAGCGGTGT  1033

Qy 1021 TTCCGGGACTTCGCTTTCCACTGAAGATGAGGAGGATGAGCGGCAGAGCACTAGCAGAGTC  1080
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Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGGATGAGCGGCAGAGCACTAGCAGAGTC  1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAAACCAGTA  1140
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Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAAACCAGTA  1153

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Db 1154 TGACTAGTCGTTGGA  1167
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RESULT 11

US-10-345-680-19

; Sequence 19, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNM_OMNI
; CURRENT APPLICATION NUMBER: US710/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(1156)

US-10-345-680-19

Query Match   99.2%; Score 1144.4; DB 15; Length 1182;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1148; Conservative 0; Mismatches 0; Indels 6; Gaps 0;

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Db   554  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 613
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Qy   601  GTCAGGGAAGACGTCGATGTCATTGAGTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   614  GTCAGGGAAGACGTCGATGTCATTGAGTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy   661  TGGTGGGACCTCTTCATGAGAGATCTCGTCTTCATCTTTGCTTCGTGTATCCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   674  TGGTGGGACCTCTTCATGAGAGATCTCGTCTTCATCTTTGCTTCGTGTATCCCTGTCCTC 733

Qy   721  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGCGTCCGGCTCCTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   734  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGCGTCCGGCTCCTTTCT 793

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db   794  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy   841  GCAGTCTTCGTTGTCGTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGCTCTGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   854  GCGGTTTTCGTTGTCGTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGCTCTGGGGG 913

Qy   901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   914  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy   961  ACCAACAGTAGCCTGAATCCCATTCCTACGGCCTTTCTTGATGAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   974  ACCAACAGTAGCCTGAATCCCATTCCTACGGCCTTTCTTGATGAAACTTCAAGCGGTGT 1033

Qy  1021  TTCCGGGACTTCTGCTTCCACTGAAGATGAGCGGCGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db  1034  TTCCGGGACTTCTGCTTCCACTGAAGATGAGCGGCGCAGAGCACTAGCAGAGTC 1093

Qy  1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||

Db  1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1153

Qy  1141  TGACTAGTCGTGGA 1154
          ||||||||||||||

Db  1154  TGACTAGTCGTGGA 1167


RESULT 13
US-10-283-975A-80
; Sequence 80, Application US/10283975A
; Publication No. US2004011792A1
; GENERAL INFORMATION:
;  APPLICANT: Ortho-Clinical Diagnostics, Inc.
;  TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
;  FILE REFERENCE: CDS 293 PCT
;  CURRENT APPLICATION NUMBER: US/10/283,975A
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/340,938
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 60/338,997
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 60/340,081
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 60/341,012
;  PRIOR FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 900
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
;  LENGTH: 1182
;  TYPE: DNA
;  ORGANISM: HUMAN
US-10-283-975A-80

Query Match             99.2%;  Score 1144.4;  DB 18;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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Db  1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1153
          ||||||||||||||||||||||||||||||||||||||||||||||||

Qy  1141  TGACTAGTCGTGGA 1154
          ||||||||||||||

Db  1154  TGACTAGTCGTGGA 1167


RESULT 12
US-10-305-720-1417
; Sequence 1417, Application US/10305720
; Publication No. US2004010136A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
;  FILE REFERENCE: PA-0002-1 CON
;  CURRENT APPLICATION NUMBER: US/10/305,720
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: 09/016,434
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 1490
;  SOFTWARE: PERL Program
; SEQ ID NO 1417
;  LENGTH: 1182
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: GenBank ID No. US20040010136A1 g532059
US-10-305-720-1417

Query Match             99.2%;  Score 1144.4;  DB 17;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy     1  ATGGACTCCCGATCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCTACCTGCCGCCCGAGCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    14  ATGGAATCCCGATTCCAGATCTTCCGCGGGGAGCCGGGGCCTACCTGCCGCCCGAGCGGCC 73

Qy    61  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    74  TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGAGCAACGGC 133

Qy   121  AGCGCCGGCTCGGAGGACGGCGCAGCTGAGCGCCGCGCCCGCACATCTCCCGCGCCATCCGGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   134  AGCGCCGGCTCGGAGGACGGCGCAGCTGAGCGCCGCGCCCGCACATCTCCCGCGCCATCCGGGTC 193

Qy   181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCGTTGGTGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   194  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCGTTGGTGGCAACTCGCTGGTC 253

Qy   241  ATGTTCGTGATCATCCGATACAAGATGAAGACAACAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   254  ATGTTCGTGATCATCCGATACAAGATGAAGACAACAGCAACCAACATTTACATATTTAAC 313

Qy   301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   314  CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   374  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy   421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   434  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCTGGACCGCTACATTGCCGTG 493

Qy   481  TGCCACCCCGTGAAGGCTTTGGACTTCCCGCACACCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   494  TGCCACCCCGTGAAGGCTTTGGACTTCCCGCACACCTTGAAGGCAAAGATCATCAATATC 553

Qy   541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCACTA 1153
         |||||||||||||||||||||||||||||||||||||||||||||||||

Qy 1141 TGACTAGTCGTGGA 1154
         ||||||||||||||
Db 1154 TGACTAGTCGTGGA 1167
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RESULT 14
US-10-318-661-1
; Sequence 1, Application US/1031866l
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-318-661-1

Query Match   98.9%;   Score 1141.4;   DB 16;   Length 1143;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC   60
         |||||  |||||| |||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC   60

Qy   61 TGCCTGCCCCCCAACAGCAGCGGCCTGTTTCCCGGCTGGGCCGGCCCGACAGCAACGGC  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCCAACAGCAGCGGCCTGTTTCCCGGCTGGGCCGGCCCGACAGCAACGGC  120

Qy  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCGGCCACATCTCCCGGCCATCCCGGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCGGCCACATCTCCCGGCCATCCCGGTC  180

Qy  181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGTGGGCAACTCGCTGGTC  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGTGGGCAACTCGCTGGTC  240

Qy  241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCAACCATTACATATTTAAC  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCAACCATTACATATTTAAC  300

Qy  301 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC  420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC  540
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Query Match   98.5%;   Score 1136.2;   DB 16;   Length 1284;
Best Local Similarity 99.7%;   Pred. No. 0;
Matches 1138;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy    2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGGCCCCGAGCGCCT   61
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGGCCCCGAGCGCCT  172

Qy   62 GCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCCGGAGCCCGACAGCAACGCGCA  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  173 GCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCCGGAGCCCGACAGCAACGCGCA  232

Qy  122 GCGGCGGCTGGAGGACGGCAGCTGGAGCCCGGCACATCTCCCCGGCATCCGGTCA  181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  233 GCGGCGGCTGGAGGACGGCAGCTGGAGCCCGGCACATCTCCCCGGCATCCGGTCA  292

Qy  182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTCA  241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  293 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTCA  352

Qy  242 TGTTCGTGATCATCCGATCACAAAGATGAAGACAGCAACCAACATTACATATTTAACC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACC  412

Qy  302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA  361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  413 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA  472

Qy  362 TGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTCCATTGATGATTACTACA  421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  473 TGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTCCATTGATGATTACTACA  532

Qy  422 ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACCATTGCCGTGT  481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  533 ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACCATTGCCGTGT  592

Qy  482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT  541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  593 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT  652

Qy  542 GCATCTGGCTGCTGTCGTCGTCATCTGTTGCATCTCTGCAATAGTCCTTGGAGGCACCCAAAG  601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  653 GCATCTGGCTGCTGTCGTCGTCATCTGTTGCATCTCTGCAATAGTCCTTGGAGGCACCCAAAG  712

Qy  602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCCT  661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  713 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCCT  772

Qy  662 GGTGGGACCTTCGTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGATCCGTCCTCA  721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  773 GGTGGGACCTTCGTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGATCCGTCCTCA  832

Qy  722 TCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGTCCGCTCCTTCTG  781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  833 TCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGTCCGCTCCTTCTG  892

Qy  782 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTGG  841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  893 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTGG  952

Qy  842 CAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTCGTGTGGAGGCTCTGGGGA  901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  953 CAGTCTTCGTTGTCTGCTGGACTCCCATTCATCCTCGTGTGGAGGCTCTGGGGA  1012

Qy  902 GCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCTGCCTAGCGTATA  961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1013 GCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCTGCCTATA  1072

Qy  962 CCAACAGTAGCCTGAATCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1073 CCAACAGTAGCCTGAATCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1132
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Qy  541 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCCAAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCCAAA  600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  660

Qy  661 TGGTGGGACCTTCGTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGATCCTCC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTTCGTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGATCCTCC  720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840

Qy  841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCTGGGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTCTTCGTTGTCTGCTGGACTCCCATTCACATATTCACATATTCTGGGG  900

Qy  901 AGACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTAGGCCTTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTAGGCCTTAGGCTAT  960

Qy  961 ACCAACAGTAGCCTGAATCCATTCCCACTGCTTCTTCCACTGCTTCTTCCACTGCTTCTTCCAGAGTC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAACAGTAGCCTGAATCCATTCCCACTGCTTCTTCCACTGCTTCTTCCACTGCTTCTTCCAGAGTC  1020

Qy 1021 TTCCGGGACTTCGCTTCTGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCACAGAGTC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCGCTTCTGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCACAGAGTC  1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy 1141 TGA 1143
          |||
Db 1141 TGA 1143
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RESULT 15
US-10-318-661-3
; Sequence 3, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR APPLICATION FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
US-10-318-661-3

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Qy    1022 TCCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTCC 1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 TCCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTCC 1192

Qy    1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAT 1141
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAG 1252

Qy    1142 G 1142
           |
Db    1253 G 1253
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Search completed: April 6, 2005, 13:18:04
Job time : 769.333 secs

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OM nucleic - nucleic search, using sw model

            GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: April 6, 2005, 12:28:42 ; Search time 4384.33 Seconds
                                            (without alignments)
                                 10018.893 Million cell updates/sec

Title: US-09-904-584-2
Perfect score: 1154
Sequence: 1 atcggactcccgatccagat........ccagtatgactagtcgtgga 1154
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_htc:*
             4: gb_est3:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	803.6	69.6	895	6	CB565888	CB565888 AGENCOURT
2	581.8	50.4	762	7	CO960667	CO960667 AGENCOURT
c 3	518.8	45.0	784	7	CO960682	CO960682 AGENCOURT
4	470.6	40.8	837	7	CF593603	CF593603 AGENCOURT
5	466.4	40.4	480	5	BX092912	BX092912
6	432.4	37.5	2405	3	AK038389	AK038389 Mus muscu
7	420	36.4	4022	3	AK043873	AK043873 Mus muscu
8	367.8	31.9	2919	3	AK038620	AK038620 Mus muscu
9	367.8	31.9	2959	3	AK079529	AK079529 Mus muscu
10	352	30.5	879	3	AY410745	AY410745 Homo sapi
11	335.6	29.1	2940	3	AK044178	AK044178 Mus muscu
12	327.4	28.4	2974	3	AK043275	AK043275 Mus muscu
13	327	28.3	3101	3	AK031926	AK031926 Mus muscu
14	325.8	28.2	879	9	AY410747	AY410747 Mus muscu
c 15	309.8	26.8	1053	9	CN504C2T	CNS04C2T Tetraodon
16	277.6	24.1	775	5	BX874804	BX874804 Tetraodon
17	274.2	23.8	787	7	CN439929	CN439929 BE04021A1
18	269.8	23.4	888	2	BF676176	BF676176 6Q2084171
19	267	23.1	917	5	BU219878	BU219878 6Q3749479
20	264.4	22.9	579	5	BP214141	BP214141 BP214141
21	263.8	22.9	579	5	BP213719	BP213719 BP213719
22	239.8	20.8	657	2	BB588668	BB588668 BB588668
23	231.2	20.0	682	9	AY410746	AY410746 Pan trogl
24	228	19.8	1176	9	AY400827	AY400827 Homo sapi
25	227.4	19.7	389	2	BB649947	BB649947 UI-M-BH3-
26	225	19.5	1176	9	AY400829	AY400829 Mus muscu
27	225	19.5	2014	9	AK046464	AK046464 Mus muscu
28	224.6	19.5	980	4	BM543468	BM543468 AGENCOURT
29	223	19.3	632	9	BB641725	BB641725 BB641725
30	219.8	19.0	1006	9	AY400676	AY400676 Mus muscu
31	217.6	18.9	784	5	BQ179053	BQ179053 UI-M-EV0-
32	215.8	18.7	750	7	CO934661	CO934661 AGENCOURT
33	214	18.5	429	7	BM342951	BM342951 fw49h03.y
34	213.8	18.5	2432	3	AK051189	AK051189 Mus muscu
35	213.2	18.5	1006	9	AY400674	AY400674 Homo sapi
36	213.2	18.5	2048	9	CR593522	CR593522 full-leng
37	213	18.5	836	9	CNS02261	CN502261 Tetraodon
38	213	18.5	866	6	CD246184	CD246184 AGENCOURT
39	211	18.3	531	7	CE517843	CE517843 tigr-gss-
40	208.6	18.1	877	9	AL211691	AL211691 Tetraodon
c 41	208.2	18.0	842	9	CNS02SC2	CNS02SKU
42	207.8	18.0	697	5	BU139251	BU139251
43	207.8	18.0	757	5	BU614716	BU614716 UI-M-EV0-
44	206.4	17.9	672	7	CO957761	CO957761 AGENCOURT
45	203.4	17.6	785	4	BI754749	BI754749 60325465

ALIGNMENTS

RESULT 1
CB565888
LOCUS   CB565888   895 bp   mRNA   linear   EST 02-APR-2003
DEFINITION AGENCOURT_12691503 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:6519213 5', mRNA sequence.
ACCESSION   CB565888
VERSION   CB565888.1 GI:29485418
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 895)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Guthrie cDNA Resource Center
            cDNA Library Preparation: Guthrie cDNA Resource Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBF001 row: f column: 09
            High quality sequence stop: 763.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6519213"
                     /tissue_type="mixed"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC 146"
                     /note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.preSV.dat
                     a. Note: this is a NIH_MGC Library."
ORIGIN

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Query Match        69.6%;  Score 803.6;  DB 6;  Length 895;
Best Local Similarity  97.0%;  Pred. No. 4.5e-200;
Matches  840;  Conservative  0;  Mismatches  24;  Indels  2;  Gaps  2;

Qy    1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCC    60
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Db    2  ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCGGGCCCTACCTGCGCCCGAGCGCC    61

Qy   61  TGCCTGCCCCCCAACAGCAGCGCCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAGCAACGGC    120
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   62  TGCCTGCCCCCCAACAGCAGCGAGCGCCGGCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCAACGGC    121

Qy  121  AGCGCGCGGCCTCGGAGGACGCGCAGCTGGAGCTGCGCGCACATCTCCCCGGCCATCCGGTC    180
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Db  122  AGCGCGCGGCCTCGGAGGACGCGCAGCTGGAGCTGCGCGCCACATCTCCCGGCCATCCCGGTC    181

Qy  181  ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTGGTGGGCAACTCGCTGGTC    240
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Db  182  ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTGGTGGGCAACTCGCTGGTC    241

Qy  241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC    300
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  242  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC    301

Qy  301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG    360
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Db  302  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG    361

Qy  361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    420
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Db  362  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    421

Qy  421  AACATGTTCACCAGCATCTCACCTTGACCATGATGAGCCGTACATTGCCGTG    480
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  422  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGTACATTGCCGTG    481

Qy  481  TGCCACCCCGTGAAGGCTTTGGACTTCCGGCACACCCTGAAGGCAAAGATCATCAATATC    540
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Db  482  TGCCACCCCGTGAAGGCTTTGGACTTCCGGCACACCCTGAAGGCAAAGATCATCAATATC    541

Qy  541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAA    600
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Db  542  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAA    601

Qy  601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCCTTGCAGTTCCCAGATGACTGACTACTCC    660
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Db  602  GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTTCCTTGCAGTTCCCAGATGACTGACTACTCC    661

Qy  661  TGGTGGGACTTCTTCATGAAGATCGCGTTCGTCCCTGATCCCTGTCCTC    720
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Db  662  TGGTGGGACTTCTTCATGAAGATCGCGTTCGTCCCTGATCCCTGTCCTC    721

Qy  721  ATCATCATGTCTGCTACACACCCTGATGATCCTGCCGTCTCCAAGAGCGTCC-GGCTCCTTTC    779
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Db  722  ATCATCATGTCTGCTACACCCTGATGATCCTGCCGTCTCCAAGAGGCGTCCGGCTCCTTTC    781

Qy  780  TGGCTCCCGAGAAAGATC-GCAACCTGGCTAGGATCACCAGGACTGGTTCCTGGTGGTG    838
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Db  782  TGGCTCCCGAGAAAGATCNGCAACCTGGCTAGGATCACCAGGACTGGTTCCCTGGTGGTG    841

Qy  839  TGGCAGTCTTGTTGTCTGGACT    864
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Db  842  GTGGGCAGTGTCTTCTTCCGTCTGGCT    867

RESULT 2
CO960667
LOCUS       CO960667        762 bp    mRNA    linear    EST 17-AUG-2004
DEFINITION  AGENCOURT 30842630 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:7389810 5', mRNA sequence.
ACCESSION   CO960667
VERSION     CO960667.1  GI:51325223
KEYWORDS    EST.
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     source          1..762
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                     /clone="IMAGE:7389810"
                     /tissue_type="mixed"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_146"
                     /note="Vector: pcDNA3.1; Site:1; multiple; Site_2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.rearranged_plates/IRBF.presV.dat
                     a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match        50.4%;  Score 581.8;  DB 7;  Length 762;
Best Local Similarity  97.1%;  Pred. No. 9.7e-142;
Matches  603;  Conservative  0;  Mismatches  17;  Indels  1;  Gaps  1;

Qy    1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCC    60
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCGGGCCCTACCTGCGCCCGAGCGCC    86

Qy   61  TGCCTGCCCCCCAACAGCAGCGCCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAGCAACGGC    120
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Db   87  TGCCTGCCCCCCAACAGCAGCGAGCGCCGGCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCAACGGC    146

Qy  121  AGCGCGCGGCCTCGGAGGACGCGCAGCTGGAGCCCGGCCCGCCCACATCTCCCCGGCCATCCCGGTC    180
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Db  147  AGCGCGCGGCCTCGGAGGACGCGCAGCTGGAGCCCGGCCCGCCCACATCTCCCGGCCATCCCGGTC    206

Qy  181  ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTGGTGGGCAACCAACATTTACATATTTAAC    240
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Db  207  ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTGGTGGGCAACCAACATTTACATATTTAAC    266

Qy  241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC    300
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  267  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC    326

Qy  301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG    360
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Db  327  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG    386

Qy  361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    420
         |||||||||||||||||||||||||||||||||||||||||||||||||
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Db    387  ATGAATTCCTGGCCTTTTGGGATGTGCTGCTGCCAAGATAGTAGTTCCATTGATTACTAC  446

Qy    421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTACATTGCCGTG  480
                ||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db    447  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGGTACATTGCCGTG  506

Qy    481  TGCCACCCCGTGAAGGCTTTGGACTTCCCGCACACCCCTTGAAGGCAAAGATCATCAATATC  540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507  TGCCACCCCGTGAAGGCTTTGGACTTCCCGCACACCCCTTGGAGGCAAAGATCATCAATATC  566

Qy    541  TGCATCTGGCT-GCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAA  599
                |||||||| ||||||||||||||||||||||||||| |||  |||||||||||||
Db    567  TGCATCTGGCTGCTGCTGTCGTCATCTGTTGTTAGCATCTCTGCTATAATCCTTGGGGAGGCGCAA  626

Qy    600  AGTCAGGGAAGAGACGTCGATGT  620
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Db    627  AATCAGGGAAGAGACTCGAAGGT  647
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RESULT 3
CO960682/c

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LOCUS        CO960682                   784 bp    mRNA      linear    EST 17-AUG-2004
DEFINITION   AGENCOURT_30842262 NIH_MGC_146 Homo sapiens cDNA clone
             IMAGE:7389810 3', mRNA sequence.
ACCESSION    CO960682
VERSION      CO960682.1  GI:51325238
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 784)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Guthrie cDNA Resource Center
             cDNA Library Preparation: Guthrie cDNA Resource Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: IRBI8   row:d   column: 04
             High quality sequence start: 214
             High quality sequence stop: 494.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:7389810"
                     /tissue_type="mixed"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_146"
                     /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.presV.dat
                     a. Note: this is a NIH_MGC Library."
ORIGIN

Query Match     45.0%;  Score 518.8;  DB 7;  Length 784;
Best Local Similarity   97.6%;  Pred. No. 3.7e-125;
Matches  537;  Conservative  0;  Mismatches  12;  Indels  1;  Gaps  1;
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Db    586  CTTGGAGGCACCAAAGTCAGGGAAGAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCA  645
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Db    577  CCTTGAGGCACCAAAGTCA-GGAAGAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCA  519

Qy    646  GATGATGACTACTCCTGGTGGGACCTTCTTCATGAAGATCTCGGGTCTTCATCTTTGCCTTC  705
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Db    518  GATGATGACTACTCCTGGTGGGACCTTCTTCATGAAGATCTCGGGTCTTCATCTTTGCCTTC  459

Qy    706  GTGATCCTGTCCTCATCATCATCTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGC  765
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Db    458  GTGATCCCTGTCCTCATCATCATCTCTGCTACACCCTGATGATCCTGCGTCTCCAAGAGC  399

Qy    766  GTCCGGCTCCTTTCTGGCTCCGGACTCTTCGTTCGTCGTCTGGACTCCCATTCACATTATTCATCCTG  825
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Db    398  GTCCGGCTCCTTTCTGGCTCCGGACTCTTCGTTCGTCGTCTGGACTCCCATTCACATATTCATCCTG  339

Qy    826  GTGGAGGCTCTGGGGAGGCACACCTCGTCTCTCCAGCTATTACTTCTGC  885
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Db    338  GTCCTGGTGGTGGTGGTGGGCAGTCTGCTGGTCGTCTGGACTCCCATTC  279

Qy    886  GTGGAGGCTCTGGGGAGGCACACCTCGTCTCTCCAGCTATTACTTCTGC  945
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Db    278  GTGGAGGCTCTGGGGAGGCACACCTCGTCTCTCCAGCTATTACTTCTGC  219

Qy    946  ATCGCCTTAGGCTATACCAACAGTAGCCTGAATCCATTCCATTTTTACGCCTTTCTGATGAA  1005
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Db    218  ATCGCCTTAGGCTATACCAACAGTAGCCTGAAATCCATTCCATTTTTTACGCCTTTCTGATGAA  159

Qy    1006 AACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAG  1065
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158  GACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAG  99

Qy    1066 AGCACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGG  1125
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Db    98   AGCACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGG  39

Qy    1126 ATGAATAAAC  1135
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Db    38   ATGATGAACC  29
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RESULT 4
CF593603

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LOCUS        CF593603                   837 bp    mRNA      linear    EST 26-SEP-2003
DEFINITION   AGENCOURT_15623822 NIH_MGC_147 Homo sapiens cDNA clone
             IMAGE:30531690 5', mRNA sequence.
ACCESSION    CF593603
VERSION      CF593603.1  GI:36347316
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 837)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
             and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: NDAM622  row: n  column: 19
             High quality sequence stop: 592.
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FEATURES        Location/Qualifiers
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                /tissue_type="Human Placenta"
                /lab_host="DH10B TonA"
                /clone_lib="NIH_MGC_147"
                /note="Organ: placenta; Vector: pBluescriptR; Site 1:
                alI-XhoI; Site 2: BamH; Oligo-dT primed using primer
                5'-TTTTTTTTTTTTTTVN-3', size-selected for average
                insert size 2.3 kb and normalized to ROT 5. This is a
                primary library enriched for full-length clones and
                constructed using the Cap-trapper method (Carninci, in
                preparation). Library constructed by M. Brownstein
                (NIMH/NHGRI, National Institutes of Health). Note: This is
                a NIH_MGC library."

ORIGIN

Query Match          40.8%;   Score 470.6; DB 7;  Length 837;
Best Local Similarity  99.2%;  Pred. No. 1.8e-112;
Matches  473;  Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCGCCCGAGCGCC    60
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Db     240 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCGCCCGAGCGCC   299

Qy      61 TGCCTGCCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCGAGCCCGACAGCAGCAACGGC   120
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Db     300 TGCCTGCCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCGAGCCCGACAGCAGCAACGGC   359

Qy     121 AGGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGGCCACATCTCCCCGGCCATCCGGTC   180
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Db     360 AGGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGGCCACATCTCCCCGGCCATCCGGTC   419

Qy     181 ATCATCACGGGGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC   240
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Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC   300
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Db     480 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC   539

Qy     301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360
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Db     540 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG   599

Qy     361 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   420
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Db     600 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   659

Qy     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCC   477
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Db     660 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCC   716
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RESULT 5
LOCUS       BX092912          480 bp    mRNA        linear    EST 23-JAN-2003
DEFINITION  BX092912 Soares placenta Nb2HP Homo sapiens cDNA clone
            IMAGp998B19190 ; IMAGE:134322, mRNA sequence.
ACCESSION   BX092912
VERSION     BX092912.1  GI:27823005
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
```

```
            Unpublished (2003)
JOURNAL     Contact: Ina Rolfs
COMMENT     RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998B19190.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES         Location/Qualifiers
     source      1..480
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGp998B19190" ; IMAGE:134322"
                 /sex="Female"
                 /dev_stage="placenta obtained at birth (full term)"
                 /lab_host="DH10B (ampicillin resistant)"
                 /clone_lib="Soares placenta Nb2HP"
                 /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                 modified polylinker; Site 1: Not I; Site_2: Eco RI; 1st
                 strand cDNA was primed with a Not I - oligo(dT) primer [5'
                 AACTGGAAGAATTCGGCGCGCCAGGAATTTTTTTTTTTTTTTT 3'],
                 double-stranded cDNA was ligated to Eco RI adaptors
                 (Pharmacia) digested with Not I and cloned into the Not I
                 and Eco RI sites of the modified pT7T3 vector. Library
                 went through one round of normalization. Library
                 constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match          40.4%;   Score 466.4; DB 5;  Length 480;
Best Local Similarity  99.8%;  Pred. No. 2e-111;
Matches  467;  Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy     687 CGTCTTCATCTTGCCTTCGTGCCTCCATCATCGTCTGCTACACCCTGAT   746
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Db       1 CGTCTTCATCTTGCCTTCGTGCCTCCATCATCGTCTGCTACACCCTGAT    60

Qy     747 GATCCTGCGTCTCAAGAGCGTCCGGTCCTTTCTGGCTCCCGAGAAAGATCGCAACCT   806
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GATCCTGCGTCTCAAGAGCGTCCGGTCCTTTCTGGCTCCCGAGAAAGATCGCAACCT   120

Qy     807 GCGTAGGAGATCACCAGACTGGTCCTGGTGGTGGTGGCAGTCTTCGTTCGTCTGTCTGGACTCC   866
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Db     121 GCGTAGGAGATCACCAGACTGGTCCTGGTGGTGGTGGCAGTCTTCGTTCGTCTGTCTGGACTCC   180

Qy     867 CATTCACATATTCATCCTGGTGGAGGCTCTGGGAGGCACCTCCCACAGCAGCAGCGTGCTCT   926
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Qy     927 CTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGATACCTCACAGTAGCCATTCT   986
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Db     241 CTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGATACCTCACAGTAGCCATTCT   300

Qy     987 CTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTCGGGACTTCTGCTTTCCACTGAA   1046
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Db     301 CTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTCGGGACTTCTGCTTTCCACTGAA   360

Qy    1047 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA   1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA   420

Qy    1107 CCTGAGGGACATCGATGGGATGAAATAAACCAGTAGTGCGTGGA   1154
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Db     421 CCTGAGGGACATCGATGGGATGAAATAAACCAGTAGTGCGTGGA   468
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RESULT 6
AK038389
LOCUS   AK038389   2405 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230002D02 product:opioid receptor, mu,
            full insert sequence.
ACCESSION   AK038389
VERSION   AK038389.1 GI:26332528
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2405)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,H., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,Y., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC);
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,

COMMENT   Fax:81-45-503-9216)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="A230002D02"
                     /sex="male"
                     /tissue_type="hypothalamus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                     (MGD|MGI:97441, GB|NM_011013, evidence: BLASTN, 99%,
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                     MSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCT
                     LTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLR
                     RITRMVLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLNPV
                     LYAFLDENFKRCFREFCIPTSSTIEQQNSARIRQNTREHPSTANTVDRTNHQPTLAVS
                     VAQIFTGYPSPTHVEKPCKSCMDRGMRNLLPDDGPRQESGEGQLGR"

ORIGIN
Query Match   37.5%; Score 432.4; DB 3; Length 2405;
Best Local Similarity   65.8%; Pred. No. 2.7e-102;
Matches 663;   Conservative   0; Mismatches 336; Indels   9; Gaps   2;

Qy   92 CCGGCTGGCCGAGCCGACAGCAACGCAGCGCCGGCTCGGAGGACCGCAGCTGGAGC 151
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Db   159 CCGACCCATGCGGTCCTAACCGACACGGGCTTGGCGGGAGCCACAGCCTGTGCCCTCAGA 218

Qy   152 CCGCGCACATCTCCCCGGCCATCTCCGGTCATCATCACGGCGTCTACTCCGTAGTGTTCG 211
             || |||||||||| |||||| ||||||||||||||| ||| ||| ||||||
Db   219 CCAGCAGCCCTTCCATGTCACAGCCATCACCATCACCATGGCCCCCTCTATTCTCATCGTGTGTG 278

Qy   212 TCGTGGGCTTGGTGGGCAACTCGCTGGTCATGTTCGTGATCATCGGATCACAAAGATGA 271
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Db   279 TAGTGGGCCTCTTTGGAAACTTCCTGGTCATGTATGTGATTGATTGTAAGATATTACCAAAATGA 338

Qy   272 AGACAGCAACCAACATTTACATATTTAACCTGGCTTTGCAGATGCTTTAGTTACTACAA 331
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Db   339 AGACTGCCACCAACATCTCACATTTCACCTTTGCTCTGGCAGATGCCTAGCCACTAGCA 398

Qy   332 CCATGCCCTTTCAGAGTACGGTCTACTTGAAGTCGATGAATTCCTGGCCTTTGGGGATGTGCTGT 391
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Db   399 CGCTGCCCTTTCAGAGTGTTAACTACCTGAGGAACGTGGCCCTTTGGAAACATCCTCT 458

Qy   392 GCAAGATAGTAATTTCCATTGATTACTACAACATGTCACAACATGTTCACCTTGACCA 451
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Qy   452 TGATGAGCGTGACCGCTACATTGCCGTGCCACCCGTGAGGGCTTTGGACTTCCGCA 511
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Db   519 CCATGAGTGTAGACCGCTACATTGCCGTCGCCCACCCGGTCAAGGCCCTGGATTTCCGTA 578

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Db   579 CCCCCGAAATGCCAAAATTGTCAATGTCTGCAACTGGATCTCTCTTCTTCGCCATTGGTC 638
          ||||||||||| ||| || ||| ||| | ||| | | | ||||||||||||||||||
Qy   572 TCTCTCGCAATAGTCCTTGGAGGCACCAAAGTCAGGAAGACGTCGATGTCATTGGTGCT 631
          |||||||| || ||||| | || |||||||| || |||||||
Db   639 TGCCCGTAATGTTCATGGCAACCACAAAATACAGGCAGGGGTC------CATAGATTGCA 692

Qy   632 CCTTGCAGTTCCCAGATGATGACTACTCCTCGGTGGGACCTCTTCATGAAGAGATCTGCGTCT 691
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Db   693 CCCTCACGTTCTCATCCCACATGGTACTGGGAGAACCTGCTC--AAAATCTGTGTCT 749

Qy   692 TCATCTTTGCCTTCGTGATCCCTGTCCTCATCATCATCATCATCGTCTGCTACACCCTGATGATCC 751
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Db   750 TCATCTTCGCCTTCATCATCGCGGTCCTCATCATCATCATCTGTGTGTTATGGACTGATGATCT 809

Qy   752 TGCGTCTCAAGAGAGGTCCGGCTCCTTCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCGTA 811
          |||| || |||| | |||| ||||| | ||||||| ||| | | |||||||||||| |
Db   810 TACGACTCAAGAGTGTCCCGCATGCTGTCCGGGCTCCAAAGAACACAGGAACCTGCGCA 869

Qy   812 GGATCACCAGCTGGTCCTGGTGGTGGCAGTCTTCGTTGTCTGCTGGACTCCCATTC 871
          |||||||| || |||||||| |||| | ||||| || |||||||||| ||
Db   870 GGATCACCCGGATGGTGCTGGTCGTGGCTGTTTCTGCTGGACCCCCATCC 929

Qy   872 ACATATTCATCCTGGTGGAGGCTCTGGGAGCACCTCCCACAGCACAGCTGCTCTCCA 931
          |||||||||||| |||| || ||| || ||||| | ||| |||||| ||| ||
Db   930 ACATCTATGTCATCATCAAAGCACTGATCATCAGATTCCAGAAACCCACTTTCCAGACTGTTT 989

Qy   932 GCTATTACTTCTGCATCGCCTTAGGCTATATACCAACAGCAGTGACTTCCATTCCTACG 991
          || || || |||| || | ||| || ||| | ||||||| |||||| |||||||| |||
Db   990 CCTGGCACTTCTGCATTGCCTTGGGTTACAACAAAACAGCTGCCTGAACCCAGTTCTTTATG 1049

Qy   992 CCTTTCTGATGAAAACTTCAAGCCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGA 1051
          || ||||||||||||| || ||| |||| || || |||||||||| ||||||| ||
Db   1050 CGTTCCTGATGAAGAAACTTCAAACGATGTTTTAGAGAGTTTCTGCATCCCAACTTCCTCCA 1109

Qy   1052 GGATGGAGCCGCAGAGCCACTAGCAGAGTCCGAAATACAGTTCAGGATC 1099
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Db   1110 CAATCGAACAGCAAAACTCTGCTCGAATCCGTCAAAACACTAGGGAAC 1157

RESULT 7
ACCESSION   AK043873
LOCUS   AK043873   4022 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830044L10 product:DELTA-TYPE OPIOID
            RECEPTOR, full insert sequence.
ACCESSION   AK043873
VERSION   AK043873.1 GI:26335979
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
    PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
    PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

TITLE   Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE   20530913
  PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4022)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="A830044L10"
                     /tissue_type="cortex"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 days neonate"
     CDS   103..1221
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                     TPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGAVVCMLQFPSPSWYWDTVTKICVF
                     LFAFVPLILITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMVLVVVGAFVVCWAP
                     IHIFVIVWTLVDINRRDPLVVALHLCIALGYANSSLNPVLYAFLDENFKRCFRQLCR
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RESULT 8
AK038620
LOCUS       AK038620        2919 bp    mRNA     linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230051A20 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK038620
VERSION     AK038620.1  GI:26332698
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,J., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2919)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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ACCESSION   AK079529
VERSION   AK079529.1 GI:26348047
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REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format

COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
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JOURNAL    sequencing pipeline with 384 multicapillary sequencer
           Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE    20530913
PUBMED     11076861
REFERENCE  4
AUTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
           FANTOM Consortium.
TITLE      Functional annotation of a full-length mouse cDNA collection
JOURNAL    Nature 409, 685-690 (2001)
REFERENCE  5
AUTHORS    The FANTOM Consortium and the RIKEN Genome Exploration Research
           Group Phase I & II Team.
TITLE      Analysis of the mouse transcriptome based on functional annotation
           of 60,770 full-length cDNAs
JOURNAL    Nature 420, 563-573 (2002)
REFERENCE  6 (bases 1 to 2959)
AUTHORS    Adachi,J., Aizawa,K., Arakawa,T., Bono,H., Carninci,P.,
           Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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           Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
           Muramatsu,M. and Hayashizaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
           Physical and Chemical Research (RIKEN), Laboratory for Genome
           Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
           RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
           Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
           URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
           Fax:81-45-503-9216)
COMMENT    cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
           Please visit our web site for further details.
           URL:http://genome.gsc.riken.jp/.
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Matches 599; Conservative  0;  Mismatches 337;  Indels  9;  Gaps  2;
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          |||||||| |||| ||||  ||  |||||| ||||| ||||||||||||  ||||||||||
Db   641  ATGAGTGTAGACCGTTATGTAGCTATCTGCCACCCATCCGTCGCCCTTGATGTTCGGACA 700

Qy   514  CCCTTGAAGGCAAAGATCATCAATATCTGCATCGGCGTCGTCATCGTTGGCATC 573
          |||| |||| ||||  ||||||||||||| |||||||  |||| ||||||||||
Db   701  TCCAGTAAAGCCCAGGCCGTTAATGTGGCCATATGGGCCCTGGCTTCGGTGGTGGTGT 760

Qy   574  TCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGACGTCGATGTCATTGAGTGCTCC 633
          ||||                                    |||  ||||||| ||||||
Db   761  CCTGTTGCCATCATGGGCCATCAGCAGT----GGAGGATGAAGAGATGAGTGCCTG 814

Qy   634  TTGCAGTTCCAGATGACTGACTACTCCTGGTGGGACCTCTTCATGAAGATCCGCGTCTTC 693
          |||||                           ||||| |  |||||||||||||||
Db   815  GTGGAGATCCCCGCCCCCCAGGA---CTATTGGGGCCCGTATTTGCCATCTGCATCTTC 871

Qy   694  ATCTTTGCCTTCGTGATCCTCTGATCCGTCCTCATCATCAGTGCTCGCACACCCTGATGATCCTG 753
          |||||| ||||||||||||||||||||||||||   |||||||| || |||||||
Db   872  CTTTTTTCCTTCATCATCCCGGTTCTGATCATCTCTGTGTGCTACAGCCTCATGATTCGA 931

Qy   754  CGTCTCAAGAGCGTCCGGCTCGTCCGGCTCTTTCTGGCTCC 813
          ||  |||||||||| ||||| ||||||| || |||||| || ||||||||||||||
Db   932  CGACTTCGTGGTGTCCGGCTCTTGAGCGGCTCTCCAGGCTCCCGAGAGAAGGACCGCAACCTGCGAGG 991

Qy   814  ATCACCAGACTGGTCCTGGTGGTGGCAGTCTTCGTTGGTGTGCTGGACTCCCATTCAC 873
          |||||| || |||||| || |||||||||| |  ||||||| ||| || ||||
Db   992  ATCACACGGCTGGTACTGGTAGTTGTGGCTGTGTTTGTGGGCTGCTGGACACCTGTGCAG 1051

Qy   874  ATATTCATCCTGGTGGAGGGCTCGGGGAGCACTCCCACAGCAGCAGGCTGCTCTCCCAGC 933
          |||||||  ||||||||||||  ||||||||| |  ||||  ||||||||||| |||||||
Db  1052  GTCTTTGTCCTGGTTCAAGGACTGGGTGTTCAGCCCGGTAGTGAGACTGCAGTAGCCATT 1111

Qy   934  TATTACTTCTGCATCGCCTTAGGCTATACCAACACAGTAGCCTGAATCCATTCTCTACGCC 993
          || ||||||||||||| ||||||  |  |||||||||| |||||||||||||| |||||||
Db  1112  CTGCGCTTCTGCACAGCCCTCGGCTATGTCAACAGCTGTCTCAACCCCATCCTCTATGCT 1171

Qy   994  TTTCTTGATGAAAACTTCAAGGCGGTGTTTCGCGTTCACTGAAGATGAGG 1053
          ||||||||||||| ||||||||||  || ||||||||| | |||||||||
Db  1172  TTCTTGGATGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTGCTGTGCTTCTGCCCTGCAC 1231

Qy  1054  ATGGAGCGCGAGCAGAGCACTAGCAGAGTCCGAAATACAGTTCAGGAT 1098
          || |||| ||||||  ||  | |    || ||||| || |||||||||
Db  1232  CGGGAGATGCAGGTTTCTGATCGTGTGCGCAGCATTGCCAAGGAT 1276
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Qy  680 AGATCTGCGTCTTCATCTTTGCTTCTCGTGATCCCTGTCCTCATCATCATCGTCTGCTACA 739
            ||||| |||| |||| |||| || ||||  |||  ||||||| ||||   |||||||||||
Db  413 CCATCTGCATCTTCCTTCCTTCCTTCATCGTCTCCCGTGCTGCTCATCTCTGTCTGCTACA 472

Qy  740 CCCTGATGATCCTGCGTCTCAAGAGACGTCCGGCTCCTTTCTGGCTCCGAGAGAAAGATC  799
            | | |||||||| || || ||  |  || |||||| ||||| || ||||| ||| ||  
Db  473 GCCTCATGATCCGGCGGCTCCGGTGGAGTCCGCCTCGTCTCCGGGTGGCAGTGAGAAGGACC 532

Qy  800 GCAACCTGGCTAGGATCACCAGACTGGTCCTGGTGCTGGTGGCAGTCTTCGTTGCTGCT  859
            | |||||| |  ||||||| |  ||||| ||||||||||||| ||| ||||| |||||||
Db  533 GGAACCTGCGGCGCATCACTCGGCTTGGTGCTGGTGGTGAGTGGCTGTGTTCGTGGGCTGCT 592

Qy  860 GGACTCCATTCACATATTCATCCTCGTGAGGAGGCTTCTGGGGAGGCCACTCCCACAGCACAG 919
            ||||  | ||  |  |||| || | | || |||| |  ||| || ||   |||||| | |
Db  593 GGACCGCCCTGTCTTCGTCGTGCTGGCCCAAGGGCTGGGGGTTCAGCCGAGCAGCGAGA   652

Qy  920 CTGCTCCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGAATC  979
            |||| |  ||| |  |||   ||||| |   | |||||| ||||||| ||| ||||  | 
Db  653 CTGCCCGGCCATTCGCGTTCTGCACGGCCTGGGCTACGTCACAGCTGCCTCAACC      712

Qy  980 CCATTCTCTACGCCTTTCTTGATGAAAAACTTCAAGCAGGTGTTTCCGGACTTCTGCTTTC 1039
            |||| || ||||| |||| |||||  ||||||| ||  | || |||||| | |||||| |
Db  713 CCATCCTTACGCCCTTCCTGGATGAGAACTTCAAGGCCTGCTTCCGCAAGTTCTGCTGTG   772

Qy 1040 CACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTCGAAATACAGTTCAGGA      1097
            ||  |  |  | | |   |||||| || || | ||||| |||  | |||| |||| 
Db  773 CATCTGCCCTGCCGCCGGGACGTGCAGGTGCTGACCGGTGCGCAGCATTGCCAAGGA    830
```

RESULT 11
AK044178
```
LOCUS       AK044178                2940 bp    mRNA        linear   HTC 03-APR-2004
DEFINITION  Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830097K10 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK044178
VERSION     AK044178.1  GI:26090219
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazana,A., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
```

RESULT 10
AY410745
```
LOCUS       AY410745                 879 bp    DNA        linear   GSS 16-DEC-2003
DEFINITION  Homo sapiens OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY410745
VERSION     AY410745.1  GI:39766713
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2  (bases 1 to 879)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..879
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>879
                     /gene="OPRL1"
                     /locus_tag="HCM3993"
ORIGIN

Query Match             30.5%;  Score 352;  DB 9;  Length 879;
Best Local Similarity   65.5%;  Pred. No. 2.9e-81;
Matches  549;  Conservative   0;  Mismatches  280;  Indels   9;  Gaps   2;

Qy  260 ACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTT  319
            |||| ||||||||||||||| ||| |  || |||||||| ||||||   ||| |  |||
Db    2 ACACCAAAATGAAGACAGCAGCCACCACCAATATTTACATCTTTACCTGGCCCGGCCACTC  61

Qy  320 TAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTG  379
            | || ||   | ||||| |||||| ||  ||| |  |||| |   | ||||||| ||| |
Db   62 TGGTCCGTGCTGACGCTGCCCTTCCCAGGGCACGGACACTCCTCCTGGGCTTCTGGCCGTTTG 121

Qy  380 GGGATGTGCGTGCGTGCAAGATAGTAATTTCCATTGATTACTACAACAATGTTCACCAGCATCT 439
            || || | |||||  ||||| | |||| | | |||||| |||||||||||| |||||| |||
Db  122 GGAATGCGCTGTGCAAGACAGTACAGTCATTGCCATTGACTACTACAACAATGTTCACCACCACCT 181

Qy  440 TCACCTTGACCATGATGAGCGTGACCCGCTACATTGCCGTGCGTGCCACCCCGTGAAGGCTT  499
            ||||| | || ||||||  | ||| | | || || ||  | |   ||||| || || ||
Db  182 TCACCCTAACTGCCATGACGTGTGATCGTGGATCGGTATGTAGCAGCCATCGTGCCC       241

Qy  500 TGGACTTCCGCACACACCCTTGAAGGCAAAGATCATCAATATCGCATCTGCTGCTGTGTCGT  559
            |||| ||||| || || || ||||| |||| | |  || ||| | | |||| ||| |||
Db  242 TCGAGTCCCGCAGTCCAGCAAAGCCCAGCGTGTCAATGTGGCCATCTGGGCCCTGGCCT      301

Qy  560 CATCTTGGTTGGCATCCTCTGCAATAGTCCTTGGAGGCCACCAAAGTCAGGGAAGACGTCGATG 619
            |   | |  | || ||   || ||| ||  ||  ||||||  |||| |||| |||| ||| 
Db  302 CTGTTGTTCGGTGTTCCCGTTGCCATCATGGCTCGGCACAGGTC------GAGGATGAAG       355

Qy  620 TCATTGAGTGCTCCTTGCAGTTCCGACGATGATGACTACTCCTGGTGGACACCTCTTCATGA 679
            | |  ||||||| |  | ||  || | |||||  |  ||| ||| || |   |||| | |
Db  356 AGATCGAGTGCCCTGGTGGAGATCCCTACCCCCAGGATTAC---TGGGGCCCCGGTGTTTG   412
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Qy    315 TGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCC 374
          ||  ||||||||  | |||| ||||||||||||||||||| ||  ||||||| || |||||
Db    483 TACCCTGGTCTTGCTGACACTGCCCTTCCAGGGCACAGACATCCTTCTGGGCTTCTGGCC 542

Qy    375 TTTTGGGGATGTGCTGTCGAAGATGAGTAGTAATTTCCATTGATTACTACAACATGTTCACCAG 434
          ||  || ||||  ||||||| |||  |||| ||||  |||| ||||| || ||||||| | |||
Db    543 ATTTGGGAATGCACTGTGCAAGACGGTCATTGCTATCGATCGACTACTACAACATGTTTACCAG 602

Qy    435 CATCTTCACCTTGACCATGATGAGCGTGACCGGCTACATTGCCGTGTGCCACCCGTGAA 494
          ||  |||| ||| || |||  || ||   || || |||  ||  ||  ||| | | |||
Db    603 CACTTTCACTTTGACTGCCATGAGTGTTATGTGCGTTAGACCGGTTATGTGGCATCATCCGTATCCG 662

Qy    495 GGCTTTGGACTTCCGACACACCCTTGAAGGCAAAGATCATCAAATATCTGCATCTGCTGCT 554
          |||||||| ||  |||| | ||  | ||||  |  || ||||  ||  ||   ||  |||
Db    663 TGCCCCTGATGTTCGGGACATCCAGTCCCAGTAAAGCCCAGGCGCGGTTAATGTGGCACCATAGTCCTG 722

Qy    555 GTCGTCATCTGTTGGCATCTGCTGCCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGACGT 614
          || ||| |||| ||||  |    ||  |      ||     ||||  || |||||| |
Db    723 GGCTTCGGTGGTTGGTGTTCCTGTTCCATGGGCTCAGCACAAGT------GGAGGA 776

Qy    615 CGATGTCATTGAGTGCTCCTGCAGTTCCCAGATGATGACTACTCCTGGTGGACCTCTT 674
          |  |||  ||  ||||  ||| || || |||  |    || ||||||  ||| || |
Db    777 TGAAGAGATCGAGTGGCCTGGTGGAGATCCCCAGGA---CTATTGGGGCCCCTGT 833

Qy    675 CATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTCATCATCGTCTG 734
          |  |||| || ||||| ||||| | ||  | |||||||| | || |||| |||||
Db    834 ATTTGCCATCGGCATCTTCCTTTTTCCTTCATCATGCCGGTTCATCATCTGTCGTCTG 893

Qy    735 CTACACCCTGATGATCCTGCGTCTCAAGAGCGGTCCGGCTCCTTTCTGGCTCCCGAGAGAA 794
          ||| |||  ||||  |    ||  ||||| |  | ||  || ||||| ||| ||||||||
Db    894 CTACAGCCTCATGATTCGACGACCTCGTGTGTCCGGCGTGCTTTCAGGCTCCCGAGAGAA 953

Qy    795 AGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTGGTCCTGGTGGTCGCAGTCTTCGTGT 854
          |  | |||| ||| | ||| ||  ||| ||| || ||| || || || ||||  ||| ||||||
Db    954 GGACCGGAACCTGCGACCATCACACGGCTACTGGTAGTTGTGGCGTACTGGTGTTGTTGTGGG 1013

Qy    855 CTGCTGGACTCCATTCACATATTCATCCGTGGAGGCTCTGGGAGGCACCTCCCACAG 914
          ||||| |||| |        |  || ||  |||| |  |||||||||  |   |||
Db    1014 CTGCTGGACACTGTCAGGCTGTCCGGTTCAAGGACTGGGTGTTCAGCCAGGTAG 1073

Qy    915 CACAGCTGCTCTCTCCAGCTATTACTTCTGACCTGCCTTAGGCTACAACAGTAGCCT 974
          ||| | |  |  |   ||| |  ||||||    |  ||   |||| || |||
Db    1074 TGAGACTGCAGTAGCCATTCTGCGCCTTCTGCACAGCCCTGGGCTATGTCAACAGTTGTCT 1133

Qy    975 GAATCCCATTCTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTG 1034
          |  |||||| |  | ||| || ||| |||| | || ||| |||  |||||
Db    1134 CAATCCCATTCTTCTTATGTCTTGGATGAGAACTTCAAGCCTGCTTTAGAAGTTCTG 1193

Qy    1035 CTTTCCACTGAAGATGAGGATGGAGCGGCAGAGTCCGAAATACAGTTCA 1094
           | |  | ||  ||||||  | ||||||  || |  ||||| || |||
Db    1194 CTGTGCTTCTGCCCTGCACCGGGGGATGCAGGTTTCTGATCGTGTCGCCGAGCATTGCCAA 1253

Qy    1095 GGAT 1098
           ||||
Db    1254 GGAT 1257
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RESULT 12
AK043275

LOCUS        AK043275    2974 bp    mRNA    linear    HTC 03-APR-2004
DEFINITION   Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
             enriched library, clone:A730079L19 product:NOCICEPTIN RECEPTOR
             (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION    AK043275
VERSION      AK043275.1    GI:26089596
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
  AUTHORS    Carninci,P. and Hayashizaki,Y.
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TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
MEDLINE      99279253
PUBMED       10349636
REFERENCE    2
AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE      20499374
PUBMED       11042159
REFERENCE    3
AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki.N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,K., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira.A. and Hayashizaki.Y.
TITLE        RIKEN integrated sequence analysis (RISA) system-384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED       11076861
REFERENCE    4
AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
TITLE        Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409, 685-690 (2001)
REFERENCE    5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE        Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    6  (bases 1 to 2974)
AUTHORS      Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,T., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
             URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.jp/
             URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1..2974
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM DB:A730079L19"
                     /db_xref="taxon:10090"
                     /clone="A730079L19"
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                     /tissue_type="cerebellum"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="7 days neonate"
     misc_feature    198..1335
                     /note="NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR)
                     (SWISSPROT|P35377, evidence: FASTY, 97.1%ID, 100%length,
                     match=1135)
                     putative"
     polyA_signal    2951..2956
                     /note="putative"
     polyA_site      2974
                     /note="putative"
ORIGIN

Query Match              28.4%;     Score 327.4;   DB 3;   Length 2974;
Best Local Similarity    63.4%;     Pred. No. 1.2e-74;
Matches  537;  Conservative   0;  Mismatches  301;  Indels   9;  Gaps   2;

Qy    252 CATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACCTGGCTTGGC 311
          ||||| ||   || | || ||| |||||||  || ||||| ||||| |||||||||||
Db    450 CAGCAGGCCACCACCAGATGAAGACTGCTACCAACATTTACATATTTAATCTGGCACTGGC 509

Qy    312 AGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCACTTGATGAATTCCTG 371
          |||| |||||||  |||||   ||||| ||||||  |||| |||||| ||| |||||||
Db    510 TGATACCCTGGTCTTGCTGCACTGCCCTTCCAGGGCACAGACATCCTTCTGGGCTTCTG 569

Qy    372 GCCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTACACATGTTCAC 431
          |||  | ||||  || ||| ||  || |    |||||  || || ||| |||||||||
Db    570 GCCATTGGGAATGCCACTGTGCAAGACGGTCATTGCTATCGACTACTACACATGTTAC 629

Qy    432 CAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGT 491
          |||| ||||||||| ||| |||||||   ||||||||| || ||||| |||  ||||||||
Db    630 CAGCACTTTCACTTGACTGCCATGATGTAGACCGTTATGTAGCTATCTGCCACCCTAT 689

Qy    492 GAAGGCTTTGGACTTCCGACACACCCTTGAAGGCAAAGATCATCAATATCTGCATCTGGCT 551
          ||| |||||||| || |||| ||||||| || |  ||  ||  ||||  |   ||||||||
Db    690 CCGTGCCCTGATGTTCGGACATCCAGTAAAGCCCAGGCCGGTTAATGTGGCCATATGGGC 749

Qy    552 GCTGCGTCATCTGTTGGACATCTCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGA 611
          || | |||  ||| ||| ||   | |||||||| |  ||||| ||  ||| |||||||
Db    750 CCTGGCTTCGGTGGTGGTTCCGTTCCATCATGGGCTCAGCACAAGT------GGA 803

Qy    612 CGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCTGGTGGACCT 671
          || |||| ||| ||| || |||  | ||||  ||||  |  |   || ||| ||||||||
Db    804 GGATGAAGAGATCGAGTGCTGCCTGGTGCCGCCCCTCCAGGA---CTATTGGGGCCCC 860

Qy    672 CTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTTCATCTTCGTCCTCTCATCATCGT 731
          ||| ||||| ||||| | ||||||| ||| |||   ||  |||||| || ||||||||||
Db    861 TGTATTTGCCATCTGCATCTTCTTTTTCCTTCATCATCCCGGTTCTGATCATCTCTGT 920

Qy    732 CTGCTACACCCTGCTGATGATCCTGCGTCTCCAAGAGCGTCCGGCTCCTTCTGCTCCCGAGA 791
          |||||||| || ||||||||||   | |||| ||||| ||  ||||| |||||||| |||
Db    921 CTGCTACAGCCTCATGATTGACGACTTCGTTGGTGTGCCTTCAGGCTCCCCGAGA 980

Qy    792 GAAAGATCGCAACCTGCGTAGGATCCGTAGGATCACCACGCTGTTGTTGTGCAGTCTTCGT 851
          || || || |||||| || |||||  ||   || ||||||  |||||||||| ||| |||
Db    981 GAAGGAGACCGGAACCTGCGACGGCATCACACGCTGGTACTGGTGTAGTTGTTGT 1040

Qy    852 TGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGGAGCACCTCCCA 911
          ||| | ||||||| |||||||||||||||||  |||| |||||||| ||||||||||||
Db    1041 GGGCTGCTGGACACCTGCAGGTCTTTGTCCTGTTCAGGGACTGGGGTTGTTCAGCCAGG 1100

Qy    912 CAGCACAGTCGCTCTCTCCAGCTATTACTTCTGCGCCTATTACTTCCAACAGTAG 971
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Qy    972 CCTGAATCCCATTCTCTACGCCTTCTTCTTGATGAAACTTCAAGCGGCGGTGTTCCGGGACTT 1031
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Db    1161 TCTCAATCCCATTCTCTATGCTTTCTTCTTGATGAGAACTTCAAGGCCTTTAGAAAGTT 1220

Qy    1032 CTGCTTTCCACTGAAGATGAGAATGGAGCGGGACAACTACAGCACTAGCAGAGTTCCGAAAATACAGT 1091
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Db    1221 CTGCTGTGCTTCTGCCCTGCACCGGAGATGCAGGTTTCTGATCGTGTGCCCTGCGCAGCATTGC 1280
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Qy      1092  TCAGGAT  1098
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Db      1281  CAAGGAT  1287


RESULT 13
AK031926
LOCUS       AK031926               3101 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
            enriched library, clone:6330500C19 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK031926
VERSION     AK031926.1  GI:26082601
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED    11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3101)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tanaka,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
```

Qy   260 ACACAAAGATGAAGACAGCAACCACATTACATATTTAACCTGGCTTGGCGATGCTT 319
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Db   2 ACACCAAGATGAAGACTGCTACCAACATTTACATATTTTAATCTGGCACTGGCTGGTGTATACCC   61

Qy   320 TAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTG 379
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Qy   620 TCATTGAGTCGTCCTTGCAGTCCCAGATGACTACTCCTGGTGGGACCCTTCATGA 679
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Qy   680 AGATCTGCGTCTTCATCTTTGCCTTCGTCATCATCATCATCCGTCTCATCATCATCTGCTCTGTCGTGCTACA 739
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Qy   740 CCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCTTCTTGCTCCAGGAGAAGATC 799
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Db   473 GCCTCATGATTCGACGACTTCGTGTGCTTCCCGGCTCGTCCCGAGAGAAGAGGACC 532

Qy   800 GCAACCTGCGTAGGATCACCAGACTGGTCCTCGTGTGGTGGCAGTCTTCGTTGTCTGCT 859
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Qy   920 CTGCTCTCCAGCTATTACTTCTGCGCTATTAGGCTATATCCGCCTTAGGCTAGCCTGAATC 979
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Qy   980 CCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCAGCGTGTTTCCGGGACTTCTGCTTTC 1039
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Qy   1040 CACTGAAGATGAGGATGGAGCGGCAGAGGAGCACTAGCAGAGGAGTCCGAAATACAGTTCAGGAT 1098
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Qy   1051 GCTACAGCCTCATGATTCGACGACTTCGTGGTGTTCGGCTCCTGCTGTGTCCCGAGAGA 1110
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Qy   1111 AGGACGGAACCTGCGACCGCCATCACACGCGGACTGGTACTGGTGGCTGTGTTTGTGG 1170
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RESULT 14
LOCUS   AY410747   879 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Mus musculus OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY410747
VERSION   AY410747.1 GI:39766715
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
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Best Local Similarity   63.5%; Pred. No. 2.3e-74;
Matches 533; Conservative   0; Mismatches 297; Indels   9; Gaps   2;

RESULT 15
CNS04C2T/c
LOCUS   CNS04C2T   1053 bp   DNA   linear   GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            09BB06 of library G from Tetraodon nigroviridis, genomic survey
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ACCESSION   AL283934
VERSION   AL283934.1 GI:8022304
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1

```
AUTHORS     Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE       Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL     Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE     20296633
PUBMED      10835645
REFERENCE   2
AUTHORS     Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Genome Res. 10 (7), 939-949 (2000)
MEDLINE     20359837
PUBMED      10899143
REFERENCE   3  (bases 1 to 1053)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
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ORIGIN

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Best Local Similarity   65.3%;   Pred. No. 3.9e-70;
Matches  587;  Conservative    8;  Mismatches  230;   Indels   74;   Gaps    7;

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Db    981 GGTACACCAAGATGAAGACCGCCACCAACATCTACACTTCAACYTGGCTYTGGCCGACG 922

Qy    317 CTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTT 376
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Qy    377 TTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACACATGTTCACCAGCA 436
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Qy    437 TCTTCACCTTGA-CCATGATGAGCGTGGA--CCGCTACATTGCCGTGCCACCCCGT-GA 493
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Qy    494 AGGCTTTGGACTTCCCGCACACCCCTTGAAGGCAAAGATCATCAATATCTGGCTGC 553
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Qy    614 TCGA---------------------------------------------------- 617
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Db    561 CCGCCAGGGAACATCGCGTGCATGCTCAGGTTCCCCAAACCGGAGAAGTACTGG--GAG 505
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Qy    670 CTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATCATCATC 729
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Qy    730 GTCTGCTACACCCTGATGATCCGTGCTCTTCAAGAGCGTCCGGCTCCTTTCTGGCTCCGA 789
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Qy    790 GAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGGTGGCAGTCTTC 849
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Db    385 GAGAAGGACCAGGAACCTCCGGCGGATCACCCGCATGGTCCTGGTGGGTGGGGCGCCTTC 326

Qy    850 GTTGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGCTCTCGGGAGCACCTCC 909
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Qy    910 CAC---AGCACAGCTGCTCTCTCCACGCTATTACTTCTGATCGGCTATACCAAC 966
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Db    265 CACAAGAACCTGCTGGTTGGCAGCTGGCACCTGTCATCGGCGCTGGGCTACATGAAC 206

Qy    967 AGTAGCCTGAATCCCATTCTACGCCTTCTTGATGAAAACTTCAAGCGGTGTTCCGG 1026
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Qy    1027 GACTTCTGCTTTCCCACTGAAGATGAGGATGGAGCGGCGCAGAGCACTAGCAGAGTTCCGAAA 1085
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Db    145 GACTTCTGCTTTCCCGCCGCGCCCGCTGAGGAGMAGAACAGCTTCTCCAGACAGAGAAA 87
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Job time : 4390.33 secs

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           Copyright  GenCore version 5.1.6
                      Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April 6, 2005, 12:28:42 ; Search time 5374.67 Seconds
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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14:  gb_vi:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1152.4	99.9	1154	9	HSU17298	U17298 Human kappa
2	1152.4	99.9	1179	6	CQ723157	CQ723157 Sequence
3	1152.4	99.9	1604	9	HUMOPRK1B	L37362 Homo sapien
4	1144.4	99.2	1182	6	AR270854	AR270854 Sequence
5	1144.4	99.2	1182	6	AX548862	AX548862 Sequence
6	1144.4	99.2	1182	9	AX774764	AX774764 Sequence
7	1144.4	99.2	1182	9	HSU11053	U11053 Human kappa
8	1141.4	98.9	1143	6	AR281679	AR281679 Sequence
9	1140.4	98.8	1142	6	A48343	A48343 Sequence 1
10	1140.4	98.8	1142	6	AR141371	AR141371 Sequence
11	1138.2	98.6	1143	9	AF498922	AF498922 Homo sapi
12	1136.2	98.5	1284	6	AR281680	AR281680 Homo sapi
13	1130.2	97.9	1143	6	AX280919	AX280919 Sequence
14	1056.8	91.6	1396	9	AY168006	AY168006 Homo sapi
15	999.4	86.6	1275	6	AR281681	AR281681 Sequence
16	994.6	86.2	1275	6	AR281682	AR281682 Sequence
17	930.6	80.6	1733	10	CPU04092	U04092 Cavia porce
18	915.6	79.3	1273	10	RATRORD	D16534 Rattus norv
19	915.6	79.3	1358	10	RATKOR1A	L22001 Rat kappa o
20	914	79.2	4742	10	RNU00442	U00442 Rattus norv
21	912.4	79.1	1288	10	S81111	S81111 kappa-opioi
22	912.4	79.1	1408	6	A68828	A68828 Sequence 5
23	912.4	79.1	1408	6	AR409589	AR409589 Sequence
24	912.4	79.1	1410	6	AR105149	AR105149 Sequence
25	912.4	79.1	1410	6	AR178399	AR178399 Sequence
26	912.4	79.1	1410	10	MUSKAPOPRE	L11065 Mouse kappa
27	912.4	79.1	2094	10	RATKOR1B	L22536 Rattus norv
28	912.4	79.1	2481	6	E08874	E08874 cDNA coding
29	912.4	79.1	2481	10	RATKOR	D16829 Rattus norv
30	869.6	75.4	1000	6	AR105156	AR105156 Sequence
31	869.6	75.4	1000	6	AR178406	AR178406 Sequence
32	632.2	54.8	757	4	PIGKOR	L49437 Sus scrofa
33	590.2	51.1	715	4	AF012105	AF012105 Sus scrof
34	580.2	50.3	1941	4	AY725197	AY725197 Taricha g
35 c	544.4	47.2	179356	2	AC083844	AC083844 Homo sapi
36 c	544.4	47.2	183519	9	AC009646	AC009646 Homo sapi
37	512.2	44.4	1454	5	AF530573	AF530573 Rana pipi
38	488.2	42.3	1477	5	AF285173	AF285173 Danio rer
39	469.2	40.7	562	11	BV209418	BV209418 OPRK1_334
40	456.8	39.6	1120	5	AY728087	AY728087 Taricha.g
41	449.6	39.0	2135	6	AR148257	AR148257 Sequence
42	449.6	39.0	2135	10	RATMUOR1A	L20684 Rattus norv
43	449.6	39.0	2397	10	RATRORB	D16349 Rattus norv
44	449.4	38.9	1387	5	AF132813	AF132813 Danio rer
45	448	38.8	1401	10	RATMOPIOID	L22455 Rat mu opio

ALIGNMENTS

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RESULT 1
HSU17298
LOCUS       HSU17298    1154 bp    mRNA    linear   PRI 14-JUL-1995
DEFINITION  Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION   U17298
VERSION     U17298.1  GI:596069
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1154)
  AUTHORS   Simonin,F., Gaveriaux-Ruff,C., Befort,K., Matthes,H., Lannes,B.,
            Micheletti,G., Mattei,M.G., Charron,G., Bloch,B. and Kieffer,B.
  TITLE     kappa-Opioid receptor in humans: cDNA and genomic cloning,
            chromosomal assignment, functional expression, pharmacology, and
            expression pattern in the central nervous system
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)
  MEDLINE   95350200
   PUBMED   7624359
REFERENCE   2  (bases 1 to 1154)
  AUTHORS   Mansson,E., Bare,L. and Yang,D.
  TITLE     Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL   Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE   94338360
   PUBMED   8060124
REFERENCE   3  (bases 1 to 1154)
  AUTHORS   Kieffer,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Superieure De
            Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Illkirch,
            67400, France
FEATURES             Location/Qualifiers
     source          1..1154
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="8"
                     /map="8q11-12"
                     /tissue_type="placenta"
     gene            1..1154
                     /gene="hKOR"
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CDS             1..1143
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                /note="G-protein coupled; transmembrane protein"
                /codon_start=1
                /product="kappa opioid receptor"
                /protein_id="AAC50158.1"
                /db_xref="GI:596070"
                /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
                EDAQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLA
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                CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMIRLRKSVRLLSGSREKDRNLRRITRIV
                LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"

ORIGIN

Query Match      99.9%;  Score 1152.4;  DB 9;  Length 1154;
Best Local Similarity   99.9%;  Pred. No. 9.9e-202;
Matches 1153;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGAGCCCTACCTGCCCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGAGCCCTACCTGCCCCCGAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCCGAGCCCGACAGCAACGGC 120
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Db     61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCCGAGCCCGACAGCAACGGC 120

Qy    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180
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Db    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCCTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCCTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
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Db    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGACATCTTCACCTTGACCATGAGCCGTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGACATCTTCACCTTGACCATGAGCCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTCTCTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTCATCGTCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGAAGAAGTCGATGTCATTGAGTGCTTCCTTCGAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGAAGAAGTCGATGTCATTGAGTGCTTCCTTCGAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAGAAGAGCCTCCGGCTCCTTCT 780
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Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAGAAGAGCCTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db    781 GGCTCCCGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy    841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGGG 900
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Db    841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGGG 900

Qy    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
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Db    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154


RESULT 2
CQ723157
LOCUS       CQ723157               1179 bp    DNA        linear   PAT 03-FEB-2004
DEFINITION  Sequence 9091 from Patent WO02068579.
ACCESSION   CQ723157
VERSION     CQ723157.1  GI:42284014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J.; Adams,M.C.; Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 9091 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1..1179
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

ORIGIN

Query Match      99.9%;  Score 1152.4;  DB 6;  Length 1179;
Best Local Similarity   99.9%;  Pred. No. 9.9e-202;
Matches 1153;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGAGCCCTACCTGCCCCCGAGCGCC 60
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGAGCCCTACCTGCCCCCGAGCGCC 70

Qy     61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCCGAGCCCGACAGCAACGGC 120
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Db     71 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCCGAGCCCGACAGCAACGGC 130

Qy    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCACATCTCCCGGTC 190

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db    191 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC 250
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SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1604)
AUTHORS        Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and
               Liu-Chen,L.-Y.
TITLE          Cloning of a human .kappa. opioid receptor from the brain
JOURNAL        Life Sci. 56, 201-207 (1995)
COMMENT        Original source text: Homo sapiens (clone d2-115) (tissue library:
               genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA
               to mRNA.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /map="8q11.2"
                     /clone="d2-115"
                     /tissue_type="brain"
                     /dev_stage="fetus"
                     /tissue_lib="genomic in lambda dash and cDNA in lambda
                     ZAPII"
     gene            1..1604
                     /gene="OPRK1"
     CDS             378..1520
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                     /codon_start=1
                     /product="kappa opioid receptor"
                     /protein_id="AAA63906.1"
                     /db_xref="GI:722618"
                     /db_xref="GDB:G00-132-651"
                     /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
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                     CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                     LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
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ORIGIN
   Query Match        99.9%;     Score 1152.4; DB 9;    Length 1604;
   Best Local Similarity   99.9%;        Pred. No. 9.9e-202;
   Matches 1153;     Mismatches   0;   Conservative   0;   Indels   1;   Gaps   0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGAGCCGGACCCTACCTGCGCCCGAGCGCC   60
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Db   378 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGAGCCGGACCCTACCTGCGCCCGAGCGCC  437

Qy    61 TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTCCCGGGCTGGGCCGAGCCGACAGCAGCGGC  120
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Db   438 TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTCCCGGGCTGGGCCGAGCCGACAGCAGCGGC  497

Qy   121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGACGCTGGAGCGCGACATCCCCGGCCATCCCGGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498 AGCGCCGGCTCGGAGGACGCGGCAGCTGGACGCTGGAGCGCGACATCCCCGGCCATCCCGGTC  557

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGTGGGCAACTCGCTGTC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGTGGGCAACTCGCTGTC  617

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTACATATTTAAC  300
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Db   618 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTACATATTTAAC  677

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTAACAACATGCCCTTTCAGAGTACGGTCTACTTG  360
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Db   678 CTGGCTTTGGCAGATGCTTTAGTTACTAACAACATGCCCTTTCAGAGTACGGTCTACTTG  737

Qy   361 ATGAATTCCTGGCCTTTTGGGATGTGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738 ATGAATTCCTGGCCTTTTGGGATGTGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC  797
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Query Match              99.2%;  Score 1144.4;  DB 6;  Length 1182;
Best Local Similarity    99.5%;  Pred. No. 2.9e-200;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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Qy    1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCCAGCGCC   60
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14  ATGGAATCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCCAGCGCC   73

Qy   61  TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTCCCGGCCGCCCGAGCCCGACAGCAGCAACGGC  120
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Db   74  TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTCCCGGCCGCCCGAGCCCGACAGCAGCAACGGC  133

Qy  121  AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCCGCGCACATCTCCCGGCCATCCCGGTC  180
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Db  134  AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCCGCGCACATCTCCCGGCCATCCCGGTC  193

Qy  181  ATCATCACCGGCGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  194  ATCATCACCGGCGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC  253

Qy  241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATATTAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  254  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATATTAAC  313

Qy  301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGGCGTCCGGCTCCTTTCT  360
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Db  314  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGGCGTCCGGCTCCTTTCT  373

Qy  361  ATGAATTCCTGGCCTTTCATTACATATTCATCTCGTGCAAGATAGTAATTTCATTGATTACTAC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  374  ATGAATTCCTGGCCTTTCATTACATATTCATCTCGTGCAAGATAGTAATTTCATTGATTACTAC  433

Qy  421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  434  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  493

Qy  481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Db  494  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  553

Qy  541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  554  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  613

Qy  601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  614  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  673

Qy  661  TGGTGGGACCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
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Db  674  TGGTGGGACCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  733

Qy  721  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
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Db  734  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  793

Qy  781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATGCGAGCGGCAGAGCACTAGCAGAGTC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  794  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATGCGAGCGGCAGAGCACTAGCAGAGTC  853

Qy  841  GCAGTCTTCGTCGTCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG  900
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Db  854  GCGGTTTCGTCGTCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG  913

Qy  901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
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Qy  961  ACCAACAGTAGCCTGAATCCCATTCTTCTTGATGAAAACTTCAAGCCGTGT  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  974  ACCAACAGTAGCCTGAATCCCATTCTTCTTACGCCTTTCTTGATGAAAACTTCAAGCCGTGT  1033

Qy 1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAAGGATGAGGATGGAGAGCGCCAGCACTAGCAGAGTC  1080
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Qy  421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  798  AACATGTTCACCAGCATCTCTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG  857

Qy  481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  858  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  917

Qy  541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  918  TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  977

Qy  601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  978  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  1037

Qy  661  TGGTGGGACCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1038  TGGTGGGACCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  1097

Qy  721  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1098  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  1157

Qy  781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATGCGAGCGGCAGAGCACTAGCAGAGTC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1158  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATGCGAGCGGCAGAGCACTAGCAGAGTC  1217

Qy  841  GCAGTCTTCGTCGTCTGGACTCCCATTCATCACATATTCATCCTGGTGGAGGCTCTGGGG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1218  GCAGTCTTCGTCGTCTGGACTCCCATTCATCACATATTCATCCTGGTGGAGGCTCTGGGG  1277

Qy  901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTCGCATTGCCTTAGGCTAT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1278  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTCGCATTGCCTTAGGCTAT  1337

Qy  961  ACCAACAGTAGCCTGAATCCCATTCTTCTTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1338  ACCAACAGTAGCCTGAATCCCATTCTTCTTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1397

Qy 1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAAGGATGAGGATGGAGAGCGCCAGCACTAGCAGAGTC  1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1398  TTCCGGGACTTCTGCTTTCCACTGAAGATGAAGGATGAGGATGGAGAGCGCCAGCACTAGCAGAGTC  1457

Qy 1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1458  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA  1517

Qy 1141  TGACTAGTCGTGGA  1154
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Db 1518  TGACTAGTCGTGGA  1531
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RESULT 4
AR270854

LOCUS       AR270854      1182 bp   DNA      linear      PAT 10-APR-2003
DEFINITION  Sequence 1417 from patent US 6500938.
ACCESSION   AR270854
VERSION     AR270854.1  GI:29702088
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1182)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1417 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1..1182
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Db    481  TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Qy    494  TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  553

Qy    541  TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTGTGGCATCTGGCATCTGAGGCACCAAA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554  TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTGTGGCATCTGGCATCTGAGGCACCAAA  613

Qy    601  GTCAGGGAAGACGTCGATGTCATGAGTGCTCCTGCAGTCCCAGATGACTACTCC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614  GTCAGGGAAGACGTCGATGTCATGAGTGCTCCTGCAGTCCCAGATGACTACTCC  673

Qy    661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCTTCATCTTTGCCTTCGTCGATCCCTGTCCTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCTTCATCTTTGCCTTCGTCGATCCCTGTCCTC  733

Qy    721  ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734  ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  793

Qy    781  GGCTCCCGAGAGAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCTCGTGGTGGTG  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794  GGCTCCCGAGAGAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCTCGGTGGTGGTG  853

Qy    841  GCAGTCTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854  GCGGTTTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG  913

Qy    901  AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914  AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  973

Qy    961  ACCAACAGTAGCCTGAATCCCATTCTTCTTCGACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974  ACCAACAGTAGCCTGAATCCCATTCTCACGCCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1033

Qy   1021  TTCCGGGACTTCGCTTTCTGCTTTCCACTGAACGATGAGAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034  TTCCGGGACTTCGCTTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC  1093

Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1153

Qy   1141  TGACTAGTCGTGA  1154
           |||||||||||||
Db   1154  TGACTAGTCGTGA  1167
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RESULT 6
AX774764
LOCUS   AX774764   1182 bp   DNA   linear   PAT 09-JUL-2003
DEFINITION Sequence 80 from Patent WO03038129.
ACCESSION   AX774764
VERSION   AX774764.1 GI:32486280
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Raponi,M.
  TITLE   Methods for assessing and treating leukemia
  JOURNAL   Patent: WO 03038129-A 80 08-MAY-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   99.2%; Score 1144.4; DB 6; Length 1182;

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Db   1034  TTCCGGGACTTCGCTTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC  1093
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Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1153

Qy   1141  TGACTAGTCGTGA  1154
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Db   1154  TGACTAGTCGTGA  1167
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RESULT 5
AX548862
LOCUS   AX548862   1182 bp   DNA   linear   PAT 26-NOV-2002
DEFINITION Sequence 147 from Patent WO02061087.
ACCESSION   AX548862
VERSION   AX548862.1 GI:25813740
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE   Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 147 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   99.2%; Score 1144.4; DB 6; Length 1182;
Best Local Similarity   99.5%;
Matches 1148;   Pred. No. 2.9e-200;
                        Mismatches   0; Conservative   0; Indels   0; Gaps   0;

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Qy      1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCGCGGCCGTCCACCTGCCCCGAGCGCC  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14  ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCGCGGCCGTCCACCTGCCCCGAGCGCC  73

Qy     61  TGCCTGCCCCCCAACAGCAGCGGCCTGCGCCTGGTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74  TGCCTGCCCCCCAACAGCAGCGGCCTGCGCCTGGTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC  133

Qy    121  AGCGCCGGCGGCTCGGAGGACGCGCAGCGCTGAGCCGCTGAGCGCGCACATCTCCCGGTC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134  AGCGCCGGCGGCTCGGAGGACGCGCAGCGCTGAGCCGCTGAGCGCGCACATCTCCCGGTC  193

Qy    181  ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTCTTGGTCGGCTTGGCAACTCGCTGGTC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194  ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTCTTGGTCGGCTTGGCAACTCGCTGGTC  253

Qy    241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAACCAACATTTACATATTTAAC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAACCAACATTTACATATTTAAC  313

Qy    301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCGGTCTACTTG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACCGGTCTACTTG  373

Qy    361  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374  ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC  433

Qy    421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCCGTACATTGCCGTG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCCGTACATTGCCGTG  493
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Best Local Similarity 99.5%; Pred. No. 2.9e-200;
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCGGCCCTACCTGCGCCCCGAGCGC   60
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Db    14 ATGGAATCCCGATTCAGATCTTCAGATCTTCCGCGGGGAGCCGGCGGCCCTACCTGCGCCCCGAGCGC   73

Qy    61 TGCCTGCCCCCAACAGCAGCCGCCGGTTTCCCGGCTGGGCCGAGCCGCGACAGCAACGGC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 TGCCTGCCCCCAACAGCAGCCGCCGGTTTCCCGGCTGGGCCGAGCCGCGACAGCAACGGC  133

Qy   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCGCCGCCACATCTCCCGGCCATCCCGGTG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCGCCGCCACATCTCCCGGCCATCCCGGTG  193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGTGGTTC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGTGGTTC  253

Qy   241 ATGTTCGTGATCATCCGATACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
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Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  373

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG  480
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Db   434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG  493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  553

Qy   541 TGCATCTGGCTGCTCGTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAA  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTCGTGTCGTCATCGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAA  613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  673

Qy   661 TGGTGGGACCTGCTCATGATGAAGAGATCGCGTCTGCATCTTTGCCTTCGTGATCCCTGTCCTC  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCCTGCTCATGATGAAGAGATCGCGTCTGCATCTTTGCCTTCGTGATCCCTGTCCTC  733

Qy   721 ATCATCATGCTGCTGCACACCCTGATGATCCTGCGTCTCAAGAGCGTCGGGTCCGGCTCCTTTCT  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATGCTGCTGCACACCCTGATGATCCTGCGTCTCAAGAGCGTCGGGTCCGGCTCCTTTCT  793

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCAGCTGCTCCTGGTGTCCTGGTGGTG  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCAGCTGCTCCTGGTGTCCTGGTGGTG  853

Qy   841 GCAGTTCGTCGTCTGCTGACTCGTGACTCCATTCATCCTGCTGATTGCGATTGCCTTAGGCTAT  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTCTGCTGACTCGTGACTCCATTCATCCTGCTGATTGCGATTGCCTTAGGCTAT  913

Qy   901 AGCACCTCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
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Db   914 AGCACCTCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  973

Qy   961 ACCAACAGTAGCCTGAATCCCAATTCTCTACGGCCTTTCTTCTTGATGAAAACTTCAAGCGGTGT  1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCAATTCCATTCCTACGGCCTTTCTTCTTGATGAAAACTTCAAGCGGTGT  1033

Qy  1021 TTCCGGGACTTCTGCTTCCCACTGAAGATGAGGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
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Db  1034 TTCCGGGACTTCTGCTTCCCACTGAAGATGAGGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1093
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Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA  1153

Qy  1141 TGACTAGTCGTGGA  1154
         ||||||||||||||
Db  1154 TGACTAGTCGTGGA  1167
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RESULT 7
HSU11053
LOCUS   HSU11053   1182 bp   mRNA   linear   PRI 22-AUG-1994
DEFINITION Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION U11053
VERSION   U11053.1 GI:532059
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1182)
  AUTHORS Mansson,E., Bare,L. and Yang,D.
  TITLE   Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE 94338360
   PUBMED 8060324
REFERENCE 2 (bases 1 to 1182)
  AUTHORS Mansson,E.
  TITLE   Direct Submission
  JOURNAL Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,
           PPD, 100 Mounatain Avenue, Murray Hill, NJ 07974, USA
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="phK1.3"
                     /tissue_type="placenta"
     gene   1..1182
                     /gene="hKOR"
     CDS   14..1156
                     /gene="hKOR"
                     /codon_start=1
                     /product="kappa opioid receptor"
                     /protein_id="AAA20985.1"
                     /db_xref="GI:532060"
                     /translation="MESPIQIFRGEPGPTCAPSACLPPNSSAWFPPWAEPDSNGSAGS
                     EDAQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLA
                     LADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAV
                     CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
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ORIGIN
Query Match   99.2%;   Score 1144.4;   DB 9;   Length 1182;
Best Local Similarity 99.5%;   Pred. No. 2.9e-200;
Matches 1148;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

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ACCESSION    AR281679
VERSION      AR281679.1  GI:29717434
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 1143)
  AUTHORS    Conklin,B.R.
  TITLE      Selective target cell activation by expression of a G
             protein-coupled receptor activated superiorly by synthetic ligand
  JOURNAL    Patent: US 6518480-A 1 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1..1143
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match         98.9%;  Score 1141.4;  DB 6;  Length 1143;
Best Local Similarity   99.9%;  Pred. No. 1e-199;
Matches 1142;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
```

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Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCGGGCCTACCTGCGCGCCCCAGCGCC 60
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Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCGGGCCTACCTGCGCGCCCCAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGCCGGCCTGGTTTCCCGGCCGCCGCCGCCGCCGCCGCC 120
Db     61 TGCCTGCCCCCAACAGCAGCGCCGGCCTGGTTTCCCGGCCGCCGCCGCCGCCGCC... 120

Qy    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGACGCGCAGCTGGAC... 180
Db    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAC... 180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGCAACTCGCTGGTC 240
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAGACAGCAGCAACCAACATTTACATATTTAAC 300
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAGACAGCAGCAACCAACATTTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db    361 ATGAATTCCTGGCCTTTTGGGGATGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTGACATTGCCGTG 480
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTGACATTGCCGTG 480

Qy    481 TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
Db    481 TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTCGTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
Db    541 TGCATCTGGCTGCTCGTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTCCCAGATGATGACTACTCC 660
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCATTGAGTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTCATGAAGATCTCGGCTTCATCTTTGCCTTCGTTGATCCCTGTCCTC 720
Db    661 TGGTGGGACCTTCATGAAGATCTCGGCTTCATCTTTGCCTTCGTTGATCCCTGTCCTC 720

Qy    721 ATCATCATGTCTGCTACACCCTGATGATCCTGCGTCTCACACCCTGATGATCCTGCGTCTC 780
Db    721 ATCATCATGTCTGCTACACCCTGATGATCCTGCGTCTCACACCCTGATGATCCTGCGTCTC 780
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Second column (right-hand alignments):

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Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGCAACTCGCTGGTC 240
Db    194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGTGGGCAACTCGCTGGTC 253

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGATGAGACAGCAGCAACCAACATTTACATATTTAAC 300
Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGATGAGACAGCAGCAACCAACATTTACATATTTAAC 313

Qy    301 CTGGCTTTGGCAGATGCTTTGAGTGTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db    314 CTGGCTTTGGCAGATGCTTTGAGTGTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db    374 ATGAATTCCTGGCCTTTTGGGGATGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCCGCTACATTGCCGTG 480
Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCCGCTACATTGCCGTG 493

Qy    481 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
Db    494 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTGGCTGCTCGTGTCGTGCTGACTCCATCTCTGGAGGCTCTGGGG 600
Db    554 TGCATCTGGCTGCTCGTGTCGTGCTGACTCCATCTCTGGAGGCTCTGGGG 613

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCCAGATGATGACTACTCC 660
Db    614 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCCAGATGATGACTACTCC 673

Qy    661 TGGTGGGACCTTCATGAAGATCTCGGCTTCATCTTTGCCTTCGTGTCCTGTCCTC 720
Db    674 TGGTGGGACCTTCATGAAGATCTCGGCTTCATCTTTGCCTTCGTGTCCTGTCCTC 733

Qy    721 ATCATCGTCTGCTACACCCTGCGCTCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
Db    734 ATCATCGTCTGCTACACCCTGCGCTCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGGTCCTGTGGTGGTG 840
Db    794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGGTCCTGTGGTGGTG 853

Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGGTGGAGGCTCTGGGG 900
Db    854 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGGTGGAGGCTCTGGGG 913

Qy    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCTCTGCATTGCCTTAGGCTAT 960
Db    914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCTCTGCATTGCCTTAGGCTAT 973

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCCGGTGT 1020
Db    974 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGCAGAGCACTAGCAGAGTC 1080
Db   1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGCAGAGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
Db   1154 TGACTAGTCGTGGA 1167
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RESULT 8
AR281679
LOCUS       AR281679  Sequence 1 from patent US 6518480.  1143 bp   DNA   linear   PAT 10-APR-2003
DEFINITION  AR281679  Sequence 1 from patent US 6518480.
```

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Qy   781  GGCTCCGGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGAGACTGGTCCTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGCTCCGGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGAGACTGGTCCTGGTGGTGGTG  840

Qy    61  TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCTGGGCCTGGGGCCGAGCCGACAGCAACGGC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCTGGGCCTGGGGCCGAGCCGACAGCAACGGC  120

Qy   841  GCAGTCTTCGTCGTCGTCGTCGTCTGGACTCCCATTCACATATTCATCCTCAGCTATTACTTCTGC  900
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Db   841  GCAGTCTTCGTCGTCGTCGTCGTCTGGACTCCCATTCACATATTCATCCTCAGCTATTACTTCTGC  900

Qy   121  AGGCCGGCTCGGAGGACGCGCAGCTGGAGCCGGAGCCGCACATCTCCCGCGCCATCCCCGGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AGGCCGGCTCGGAGGACGCGCAGCTGGAGCCGGAGCCGCACATCTCCCGCGCCATCCCCGGTC  180

Qy   901  AGCACCTCCCACAGCAGCAGCTGCTTCTCCAGCTATTACTTCTGCATTCTGCCTTAGGCTAT  960
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Db   901  AGCACCTCCCACAGCAGCAGCTGCTTCTCCAGCTATTACTTCTGCATTCTGCCTTAGGCTAT  960

Qy   181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240

Qy   961  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT  1020

Qy   241  ATGTTCGTGATCATCGATACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATGTTCGTGATCATCGATACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080

Qy   301  CTGGCCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTGGCCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC  420

Qy   1141 TG  1142
          ||
Db   1141 TG  1142

Qy   421  AACATGTTCACCAGCATCTTCACCTTGACCATGAGGAGCGTGGACCGCTACATTGCCGTG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AACATGTTCACCAGCATCTTCACCTTGACCATGAGGAGCGTGGACCGCTACATTGCCGTG  480

Qy   481  TGCCACCCGTGAAGGCTTTGGACTTCGTGTCATCGTGGCATCATTCTGCAATAGTCATCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TGCCACCCGTGAAGGCTTTGGACTTCGTGTCATCGTGGCATCATTCTGCAATAGTCATCA  540

Qy   541  TGCATCTGGCTGCTGTCGTCATCGTGATGTCATTGAGTGCTCCTCCAGTTCCAGTCAGTGACTACTCC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TGCATCTGGCTGCTGTCGTCATCGTGATGTCATTGAGTGCTCCTCCAGTTCCAGTCAGTGACTACTCC  600

Qy   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTCCAGTTCCAGTCAGTGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTCCAGTTCCAGTCAGTGACTACTCC  660

Qy   661  TGGTGGGACCTCTTCATGAAGATCGCGCTTCATCTTTGCCTTCGTGATCCCTCGTCCTC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TGGTGGGACCTCTTCATGAAGATCGCGCTTCATCTTTGCCTTCGTGATCCCTCGTCCTC  720

Qy   721  ATCATCATCGTCTGCTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATCATCATCGTCTGCTCACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
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RESULT 9

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A48343
LOCUS       A48343                   1142 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 1 from Patent WO9601898.
ACCESSION   A48343
VERSION     A48343.1  GI:2302133
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Kieffer,B. and Simonin,F.
  TITLE     HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
  JOURNAL   Patent: WO 9601898-A 1 25-JAN-1996;
            UNIV PASTEUR (FR)
COMMENT     Other publication FR 2722209 960112.
FEATURES             Location/Qualifiers
     source          1..1142
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             1..>1142
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA03102.1"
                     /db_xref="GI:2302134"
                     /translation="MDSPIQIFRGEPGPTCAPSACLPNSSAWFPGWAEPDSNGSAGS
                     EDAQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLA
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                     CHPVKALDFRTPLKAKIINICIWLLSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMIRLKSVRLLSSSREKDRNLRRITRLV
                     VVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                     ENPFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"
ORIGIN
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Query Match             98.8%;  Score 1140.4;  DB 6;  Length 1142;
Best Local Similarity   99.9%;  Pred. No. 1.6e-199;
Matches 1141;  Mismatches    0;  Conservative    0;  Indels    1;  Gaps    0;
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Qy     1  ATGGGACTTCCCGATCCAGATCTTCCCGCGGGAGCCCGGGAGCCCTACCTGGCCCCGAGCGCC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGGGACTTCCCGATCCAGATCTTCCCGCGGGAGCCCGGGAGCCCTACCTGGCCCCGAGCGCC  60

Qy    61  TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCTGGGCCTGGGGCCGAGCCGACAGCAACGGC  120
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Db   1141 TG 1142

RESULT 10
AR141371
LOCUS   AR141371   1142 bp   DNA   linear   PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6146835.
ACCESSION   AR141371
VERSION   AR141371.1 GI:15100887
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1142)
  AUTHORS   Kieffer,B. and Simonin,F.
  TITLE   Human kappa opioid receptor, nucleic acids and uses thereof
  JOURNAL   Patent: US 6146835-A 1 14-NOV-2000;
FEATURES   Location/Qualifiers
     source   1..1142
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match   98.8%; Score 1140.4; DB 6; Length 1142;
Best Local Similarity 99.9%; Pred. No. 1.6e-199;
Matches 1141; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60

Qy   61 TGCCTGCCCCCAACAGCAGCAGCCGCTGGTTTCCCGGCTGGGCCGGAGCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCAGCCGCTGGTTTCCCGGCTGGGCCGGAGCCGACAGCAACGGC 120

Qy   121 AGCGCCGGCTCCGAGGACGCGGCAGCTGAGCCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCCGAGGACGCGGCAGCTGAGCCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGACATTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGACATTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACACAACCATCGCCTTTCAGATGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACACAACCATCGCCTTTCAGATGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTGCAAGATAATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTGCAAGATAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTCGTCTGTCGTGGCATCTCGTTGACTCCTGCAATAGTCCTTGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTCGTCTGTCGTGGCATCTCGTTGACTCCTGCAATAGTCCTTGAGGCACCAAA 600

Qy   601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGACTGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGACTGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTTCAAGAGCGTCCGGCTCCTTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCGGTCTGGTCGTGGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCGGTCTGGTCGTGGTGGTG 840

Qy   841 GCAGTCTCGTCGTCGTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTCGTCGTCGTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCACAGACAGCTGCTCTCCAGCTATTACTTCGTCATTGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGACAGCTGCTCTCCAGCTATTACTTCGTCATTGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCACGCCTTCTTGATGAAAACTTCAAGCGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCACGCCTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCAGACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCAGACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGAGCTGCTCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGAGCTGCTCTGCTTACCTGAGGGACATCGATGGGGATGAATAAACCAGTA 1140

Qy   1141 TG 1142
           ||
Db   1141 TG 1142

RESULT 11
AF498922
LOCUS   AF498922   1143 bp   mRNA   linear   PRI 01-MAY-2002
DEFINITION Homo sapiens opioid receptor kappa (OPRK1) mRNA, complete cds.
ACCESSION   AF498922
VERSION   AF498922.1 GI:20379019
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1143)
  AUTHORS   Puhl,H.L., Ikeda,S.R. and Aronstam,R.S.
  TITLE   Direct Submission
  JOURNAL   Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
            Institute, One Guthrie Square, Sayre, PA 18840, USA
FEATURES   Location/Qualifiers
     source   1..1143
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="brain"
     gene   1..1143
                     /gene="OPRK1"
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                     /gene="OPRK1"
                     /note="G protein coupled receptor"
                     /codon_start=1
                     /product="opioid receptor kappa"
                     /protein_id="AAM21070.1"
                     /db_xref="GI:20379020"
                     /translation="MESPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
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                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                     LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                     ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"

ORIGIN

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Query Match          98.6%;   Score 1138.2;  DB 9;  Length 1143;
Best Local Similarity  99.7%;   Pred. No. 4e-199;
Matches 1140;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCC 60
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCGCGCCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCGCGCCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC 120

Qy  121 AGCGCCGGCTCGGAGGACCGCAGCTGGACCGGGCCCGCCCAGCGCGGGTCCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGCGCCGGCTCGGAGGACCGCAGCTGGACCGGGCCCGCCCAGCGCGGGTCCCCGGTC 180

Qy  181 ATCATCACGGCGGGGTCTACTCCGTAGTGTTCGTCGTGGGTGGGCAACTCGCTGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCGGGGTCTACTCCGTAGTGTTCGTCGTGGGTGGGCAACTCGCTGGTC 240

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy  301 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy  361 ATGAATTCCTGGCCTTTGGGATGTGCTGTCGTCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTGGGATGTGCTGTCGTCAAGATAGTAATTTCCATTGATTACTAC 420

Qy  421 AACATGTTCACCAGACATCTTCACCTTGACCATGAGCGTGGACCGCTACCATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGACATCTTCACCTTGACCATGAGCGTGGACCGCTACCATTGCCGTG 480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCTGAAGGCAAAGATCATCAATATC 540

Qy  541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCTGGAGGCACCAAA 600
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCTGGAGGCACCAAA 600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy  661 TGGTGGGACCCTTCTTCATGAGAGATCGCGTCTTCCATCTTTGCCTTCGTTCGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCCTTCTTCATGAGAGATCGCGTCTTCCATCTTTGCCTTCGTTCGTCCTC 720

Qy  721 ATCATCATCGTCTGCTACACACCCTGCGTCTACACCTGCGTCTCTCGCGTCCGGCTCCTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACACCCTGCGTCTACACCTGCGTCTCTCGCGTCCGGCTCCTT 780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCACCAGACTGGTCCTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCACCAGACTGGTCCTGGTGGTG 840

Qy  841 GCAGTTCGTCGTCGTCTGACTCCAATCCAATTCACAGATTCATCCTGTGGAGGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTTCGTCGTCGTCTGACTCCAATCCAATTCACAGATTCATCCTGTGGAGGGCTCTGGGG 900

Qy  901 AGCACCTCCACAGACACAGCTGCTTCTCCAGCTATTACTTCTGCATTGCCGTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGCACCTCCACAGACACAGCTGCTTCTCCAGCTATTACTTCTGCATTGCCGTTAGGCTAT 960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTGATGAATGAAAACTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTGATGAATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCGCAGAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGTGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGTGATGAATAAACCAGTA 1140

Qy 1141 TGA 1143
          ||
Db 1141 TGA 1143
```

RESULT 12

```
AR281680
LOCUS       AR281680                1284 bp    DNA       linear   PAT 10-APR-2003
DEFINITION  Sequence 3 from patent US 6518480.
ACCESSION   AR281680
VERSION     AR281680.1  GI:29717435
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1284).
AUTHORS     Conklin,B.R.
TITLE       Selective target cell activation by expression of a G
            protein-coupled receptor activated superiorly by synthetic ligand
JOURNAL     Patent: US 6518480-A 3 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1..1284
                     /organism="unknown"
                     /mol_type="genomic DNA"
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ORIGIN

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Query Match          98.5%;   Score 1136.2;  DB 6;  Length 1284;
Best Local Similarity  99.7%;   Pred. No. 9.4e-199;
Matches 1138;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCCT 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCCT 172

Qy   62 GCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAGCAACGGCA 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  173 GCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAGCAACGGCA 232

Qy  122 GCGCCGGCTCGGAGGACCGCAGCTGGACCGGGCCCGCCCAGCTCCCGGCCATCCCGGTCA 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  233 GCGCCGGCTCGGAGGACCGCAGCTGGACCGGGCCCGCCCAGCTCCCGGCCATCCCGGTCA 292

Qy  182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTGGTGGGCAACTCGCTGGTCA 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  293 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTGGTGGGCAACTCGCTGGTCA 352

Qy  242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC 301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC 412

Qy  302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  413 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 472

Qy  362 TGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  473 TGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA 532

Qy  422 ACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGCTACCATTGCCGTGT 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  533 ACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGCTACCATTGCCGTGT 592

Qy  482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT 541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Matches 1135; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db   593  GCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCT  652

Qy     1  ATGGACTCCCGATCCAGATCTTCGTCGTCGTTGGCATCTGTTGGCAATAGTCCTTGGAGGCACCCAAG   60
          |||||  |||||| ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db     1  ATGGAATCCCGATTCAGATCTTCGTCGTCGTTGGCATCTGTTGGCAATAGTCCTTGGAGGCCCAGCGGC   60
Db   653  GCATCTGGCTGTCGTGTCGTCGTTGGCATCTGTTGGCAATAGTCCTTGGAGGCCCAGCGGC  712

Qy    61  TGCCTGCCCCCAACAGCAGCAGCGGCCGGCTGGTTCCCGGCGGTTCCCGGCGGCCGACAGCAGCAACGGC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TGCCTGCCCCCAACAGCAGCAGCGGCCGGCTGGTTCCCGGCGGTTCCCGGCGGCCGACAGCAGCAACGGC  120

Qy   121  AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCACGCCGCGCACATCTCCCCGGCCATCCGGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCACGCCGCGCACATCTCCCCGGCCATCCGGGTC  180

Qy   181  ATCATCACGGCGGTCTACTCCGTCTCCGAGAGCGTCGGCTTCGTCGTGTGGGCAACTCGCTGGTC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATCATCACGGCGGTCTACTCCGTCTCCGAGAGCGTCGGCTTCGTCGTGTGGGCAACTCGCTGGTC  240

Qy   241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300

Qy   301  CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACATGTTGCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCGCATTGATTACTACAC  420

Qy   421  AACATGTTCACCAGCATCTTCACCTGACCATGATGAGCGTGACCGCTCACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AACATGTTCACCAGCATCTTCACCTGACCATGATGAGCGTGACCGCTCACATGCCGTG  480

Qy   481  TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGGACTTCTGTCGTTGGACTTCGTGTCATCAATATC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGGACTTCTGTCGTTGGACTTCGTGTCATCAATATC  540

Qy   541  TGCATCTGGCTGTCGTGTCGTCATCGTGTTGGCATCTGGCATCGTGTTGGAGGCACCAGTAT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TGCATCTGGCTGTCGTGTCGTCATCGTGTTGGCATCTGGCATCGTGTTGGAGGCACCAGTAT  600

Qy   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCCTTCGTCTTTGCCTTCGTGTCCCGTCCTC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCCTTCGTCTTTGCCTTCGTGTCCCGTCCTC  660

Qy   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCTTGCCTTCGTCTTGCCTTCTT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCTTGCCTTCGTCTTGCCTTCTT  720

Qy   721  ATCATCATGTCTGCTACACCCTGCGTCTGATGATCCTGATGATCCTCGGCTCCTTTCT  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATCATCATGTCTGCTACACCCTGCGTCTGATGATCCTGATGATCCTCGGCTCCTTTCT  780

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCGGTCTCGGTGGTCCTCGGTGGTGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCGGTCTCGGTGGTCCTCGGTGGTGTG  840

Qy   841  GCAGTCTTCGTGTCTCGTGCAGCTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCCGTTTCGTGTCTCGTGCAGCTCCATTCCACATATTCATCCTGGTGGAGGCTCTGGGG  900

Qy   901  AGCACCTCCCAGCAGACAGCTGCTCCTCCAGCTATTACTTCTCCCAGCTATTACTTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AGCACCTCCCAGCAGACAGCTGCTCCTCCAGCTATTACTTCTCCCAGCTATTACTTAGGCTAT  960

Qy   961  ACCAACAGTAGCCTGCTTTCTCGCGCCTTTCTTGATGAAAAACTTCAAGCGGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  ACCAACAGTAGCCTGCTTTCTCGCGCCTTTCTTGATGAAAAACTTCAAGCGGTGT  1020

Qy  1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCAGCAGCACTAGCAGAGTC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCAGCAGCACTAGCAGAGTC  1080

Qy  1081  TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGGACTTCTGTCCTCA  1081
          ||||||||||||||||||||||
Db  1133  GGCTCCGGGACTTCTGCTTTCCACTGAAGATCGCAAGAGAAAGATCGCAAGAGAAAGATCGCAAGAGAGTC  1192

Qy  1082  GAAATACAGTTCAGGATCTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGGAATAAAACCAGTAT  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1193  GAAATACAGTTCAGGATCTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGGAATAAAACCAGTAG  1252

Qy  1142  G  1142
          |
Db  1253  G  1253
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RESULT 13
AX280919

LOCUS   AX280919   1143 bp   DNA   linear   PAT 02-NOV-2001
DEFINITION Sequence 542 from Patent WO0177172.
ACCESSION   AX280919
VERSION   AX280919.1 GI:16608215
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.
  TITLE   Non-endogenous, constitutively activated known g protein-coupled
            receptors
  JOURNAL   Patent: WO 0177172-A 542 18-OCT-2001;
            Arena Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1143
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   97.9%; Score 1130.2; DB 6; Length 1143;
Best Local Similarity   99.3%; Pred. No. 1.2e-197;

Db 495 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 554
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 361 ATGAATTCCTGGCCTTTGGGGATGCTGTGCAAGATAGTAGTTCCATTGATTACTAC 420
         |||||||||||||||||||||||||||||||||||||||||||||||

Db 555 ATGAATTCCTGGCCTTTGGGGATGCGTGTGCAAGATAGTAGTAATTCATTGATTACTAC 614

Qy 421 AACATGTTCACCAGATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 615 AACATGTTCACCAGATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 674

Qy 481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 675 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 734

Qy 541 TGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 735 TGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 794

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCAGATGATGACTACTCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 795 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTCCAGATGATGACTACTCC 854

Qy 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 855 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 914

Qy 721 ATCATCATCTGCTGCACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 915 ATCATCATCTGCTGCACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 974

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGAATCACCAGACTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 975 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGAATCACCAGACTGGTGGTG 1034

Qy 841 GCAGTTCTTCGTCGTCGTGGACTCCCATTCACATATTCACATCCTGGTGGAGGCTCTGGGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1035 GCAGTTCTTCGTCGTCGTGGACTCCCATTCACATATTCACATCCTGGTGGAGGCTCTGGGG 1094

Qy 901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCTCTGCCTTTAGGCTAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1095 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCTCTGCCTTTAGGCTAT 1154

Qy 961 ACCAACAGTAGCCTGAATCCCATCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1155 ACCAACAGTAGCCTGAATCCCATCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1214

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1215 TTCCGGGACTTCTGCTTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1274

Qy 1081 CGAAATACAGTTCAGGATCCTCGCTTACCTGAGGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1275 CGAAATACAGTTCAGGATCCTCGCTTACCTGAGGGGACATCGATGGGATGAATAAACCAGTA 1334

Qy 1141 TGACTAGTCGTGGA 1154
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Db 1335 TGACTAGTCGTGGA 1348

RESULT 15
AR281681

LOCUS   AR281681   1275 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6518480.
ACCESSION   AR281681
VERSION   AR281681.1 GI:29717436
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1275)
  AUTHORS   Conklin,B.R.
  TITLE   Selective target cell activation by expression of a G
            protein-coupled receptor activated superiorly by synthetic ligand

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Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy 1141 TGA 1143
         |||

Db 1141 TGA 1143

RESULT 14
AY168006

LOCUS   AY168006   1396 bp   mRNA   linear   PRI 25-DEC-2002
DEFINITION Homo sapiens DRG kappa 1 splice variant KOR 1A mRNA, complete cds,
            alternatively spliced.
ACCESSION   AY168006
VERSION   AY168006.1 GI:27373027
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1396)
  AUTHORS   Lu,L.D. and Mansson,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371
            Phoenixville Pike, Malvern, PA 19355, USA
FEATURES   Location/Qualifiers
     source   1..1396
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS   237..1337
                     /note="opioid receptor kappa 1A; alternatively spliced"
                     /codon_start=1
                     /product="DRG kappa 1 splice variant KOR 1A"
                     /protein_id="AAN87342.1"
                     /db_xref="GI:27373028"
                     /translation="MDSPIQIFRGEPGEPTCAPSACLPNSSAGSEDAQLEPAHISPAI
                     PVITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQS
                     TVYLMNSWPFGDALCKIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLK
                     AKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWWDLFMKICVFI
                     FAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLVLVVVAVFVVCWTPI
                     HIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPL
                     KMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"
ORIGIN
Query Match   91.6%; Score 1056.8; DB 9; Length 1396;
Best Local Similarity   96.2%; Pred. No. 3.7e-184;
Matches 1110; Conservative   0; Mismatches   2; Indels   42; Gaps   1;

Qy   1 ATGGGAGCTCCCGATCTTCCGCGGGGAGCCCGGCCCGGCCCTACCTGCGCCCGAGCGCC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 237 ATGGGAGCTCCCGATCTTCCGCGGGGAGCCCGGCCCGGCCCTACCTGCGCCCGAGCGCC 296

Qy 61   TGCCTGCGCCCCCAACAGCAGCGCGCTGGTTCCCGGCTGGGCGTGGGCGAGCCGACAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||

Db 297 TGCCTGCGCCCCCAACA------------------------------------GC 314

Qy 121 AGCGCCGGCTCGGAGGACGCGCGAGCGCCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 315 AGCGCCGGCTCGGAGGACGCGCGAGCGCCGCAGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC 374

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 375 ATCATCACGGCGGTCTACTCCGTAGTTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 434

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 435 ATGTTCGTGATCATCCGATACACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 494

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

JOURNAL   Patent: US 6518480-A 5 11-FEB-2003;
FEATURES
     source   1..1275
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   86.6%; Score 999.4; DB 6; Length 1275;
Best Local Similarity 93.0%; Pred. No. 1.3e-173;
Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

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Qy       2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCCCCGAGCGCCT    61
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Db     113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCCCCGAGCGCCCT   172

Qy      62 GCCTGCCCGCCCCCAACAGCAGCCGCCTGGTTTCCCGGCTGGGCCGAGCAACAGCGGCA   121
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Db     173 GCCTGCCCGCCCCCAACAGCAGCCGCCGCGCTGGTTTCCCGGCTGGGCCGAGCAACAGCGGCA  232

Qy     122 GCGCCGGCTCGGAGGACGCGGCAGCTGGCCCGGCCCGCGCACATCTCCCCGCCATCCCGGTCA   181
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Db     233 GCGCCGGCTCGGAGGACGCGGCAGCTGGCCCGGCCCGCGCACATCTCCCGCGGCCATCCCGGTCA  292

Qy     182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTCA   241
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Qy     242 TGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAACC   301
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Db     353 TGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAACC  412

Qy     302 TGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA   361
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Qy     362 TGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA   421
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Qy     422 ACATGTTCACCAGCACATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGT   481
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Db     533 ACATGTTACCAGCACATCTTCACCTTGACCATGATGAGTGTGGACCGTTACATTGCCGTGT  592

Qy     482 GCCACCCCGTGAAGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT   541
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Qy     542 GCATCTGGCTGCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAG   601
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Qy     602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCCT   661
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Qy     662 GGTGGGACCTCTTCATGAAGATCTGCCTCTTCATCTTTGCCTTCGTCCTGTCCTCA   721
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Qy     722 TCATCATCGTCTGCTACACCCTGATGATCCTGCGTAGGATCCGCTCCAAGAGCGTCCGGCTCCTTTTCTG   781
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Qy     782 GCTCTGCTGGACTCCATTCACATATTCATCACCGAGACTGTGGTGGTGG   841
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Qy     842 CAGTCTTCGTCTGCTGGACTCCGTTCATCCTCGGTGGAGGCTCTGGGGA   901
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Db     944 CAGTCTTCGTCTGCTGGACTCCCATTCATCCTCGGTGGAGGCTCTGGGGA   1003

Qy     902 GCACCTCCCACGACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATCGCT   961
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Db    1004 GCACCTCCCACGACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATCGCT   1063

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Qy    1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTCC   1081
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Db    1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTCC   1183

Qy    1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGGATGGACCATCGATGGATGAATAAACCAGTAT   1141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1184 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACCATCGATGGGATGAATAAACCAGTAG   1243

Qy    1142 G   1142
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Db    1244 G   1244
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Search completed: April 6, 2005, 18:22:08
Job time : 5377.67 secs

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             GenCore version 5.1.6
             Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April  6, 2005, 12:28:42 ; Search time 700.667 Seconds
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Title:       US-09-904-584-3
Perfect score: 1154
Sequence:    1 atggactcccgatccagat.........ccagtatgactagtcgtgga 1154

Scoring table: IDENTITY NUC
             Gapop 10_0 , Gapext 1.0

Searched:    4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:    8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_16Dec04:*
         1:  geneseqn1980s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1154	100.0	1154	12	ADN30507	Adn30507 Human kap
2	1152.4	99.9	1154	12	ADN30505	Adn30505 Human kap
3	1152.4	99.9	1154	13	ADR44858	Adr44858 Human kap
4	1150.8	99.7	1154	12	ADN30506	Adn30506 Human kap
5	1150.8	99.7	1154	12	ADN30510	Adn30510 Human kap
6	1150.8	99.7	1154	12	ADN30508	Adn30508 Human kap
7	1150.8	99.7	1154	12	ADN30511	Adn30511 Human kap
8	1150.8	99.7	1154	12	ADN30509	Adn30509 Human kap
9	1144.4	99.2	1182	8	ABZ42678	Abz42678 Human opi
10	1144.4	99.2	1182	10	AAD58490	Aad58490 Human kap
11	1144.4	99.2	1182	10	ADE84861	Ade84861 Farnesyl
12	1144.4	99.2	1182	10	ACA56819	Aca56819 Human sig
13	1144.4	99.2	1182	12	ADI56615	Adi56615 Human pol
14	1141.4	98.9	1143	2	AAT90998	Aat90998 Human kap
15	1140.4	98.8	1142	2	AAT12550	Aat12550 Human kap
16	1136.2	98.5	1284	2	AAT90999	Aat90999 Human kap
17	1136.2	98.5	1284	11	ADL90106	Adl90106 cDNA enco
18	1133.4	98.2	1143	12	ADO30011	Ado30011 Human GPC
19	1130.2	97.9	1143	5	ABI98011	Abi98011 Non-endog
20	999.4	86.6	1275	2	AAT92601	Aat92601 Human kap
21	999.4	86.6	1275	11	ADL90108	Adl90108 Human kap
22	994.6	86.2	1275	11	ADL90110	Adl90110 Human kap
23	979.4	84.9	1875	11	ADL90116	Adl90116 Human kap
24	963.4	83.5	1875	11	ADL90118	Adl90118 Human kap
25	912.4	79.1	1408	2	AAV49254	Aav49254 Mouse kap
26	912.4	79.1	1410	2	AAQ75926	Aaq75926 Mouse kap
27	912.4	79.1	1410	13	ADR44860	Adr44860 Mouse kap
28	912.4	79.1	2481	13	AAQ86725	Aaq86725 Mammalian
29	912.4	79.1	2481	13	ADR44862	Adr44862 Rat kappa
30	901.4	78.1	1143	12	ADO30301	Ado30301 Mouse GPC
31	877.8	76.1	1911	11	ADL90120	Adl90120 Human kap
32	868	75.2	1000	2	AAQ75931	Aaq75931 Human kap
33	449.6	39.0	2135	5	AAF85416	Aaf85416 Nucleotid
34	448	38.8	1401	13	ADR44848	Adr44848 Rat mu-op
35	448	38.8	1618	2	AAQ89222	Aaq89222 Rat mu op
36	448	38.8	1618	3	AAQ89223	Aaq89223 Transcrip
37	448	38.8	1618	3	AAA59499	Aaa59499 cDNA enco
38	445	38.6	2070	2	AAQ79199	Aaq79199 Rat mu-su
39	440	38.1	9426	13	ADR44835	Adr44835 FIV opioi
40 c	440	38.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
41	440	38.1	10472	13	ADR44876	Adr44876 Plasmid p
42	438	38.0	2162	2	AAV61994	Aav61994 Human mu-
43	437.8	37.9	1464	10	ADG42250	Adg42250 Mu-opioid
44	436.4	37.8	1200	13	ADR44830	Adr44830 Human HUM
45	436.4	37.8	1200	13	ADR44837	Adr44837 HUMOR mut

ALIGNMENTS

```
RESULT 1
ADN30507
ID   ADN30507 standard; cDNA; 1154 BP.
XX
AC   ADN30507;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C948T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          replace(948,C)
FT                   /*tag= a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
```

```
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 3; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful for
CC   determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C948T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match         100.0%;  Score 1154;  DB 12;  Length 1154;
Best Local Similarity  100.0%;  Pred. No. 2.7e-273;
Matches 1154;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGAGCGGC 60
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Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGAGCGGC 60

Qy     61 TGCCTGCCCCCAACAGCAGGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
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Qy    121 AGCGCCGGCTCGGAGGACGGCGGAGCAGCGCCGCCCGCGCACATCTCCCGCGGCCATCCCGGTC 180
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Db    121 AGCGCCGGCTCGGAGGACGGCGGAGCAGCGCCGCCCGCGCACATCTCCCGCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCGGTCTCACTCCGTAGTGTTCGTCGTGGCTTGGTCGGTCGGCAACTCGCTGGTC 240
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Db    181 ATCATCACGGCGGTCTCACTCCGTAGTGTTCGTCGTGGCTTGGTCGGTCGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCACCAACATTTACATATTTAAC 300
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Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCACCAACATTTACATATTTAAC 300

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Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGAACCGGCTACATTGCCGTG 480
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Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGAACCGGCTACATTGCCGTG 480
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Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAAATATC 540
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Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
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Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTCATGAAGATCGCGTTCTTCATCTTTGCCTTCGTGTATCCCTGTCCTC 720
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Db    661 TGGTGGGACCTTCATGAAGATCGCGTTCTTCATCTTTGCCTTCGTGTATCCCTGTCCTC 720

Qy    721 ATATCATCGTCTGCTACACCCTGATGATCCTGGTCTCAAGAGCGTCCGGCGTCCTTTCT 780
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Db    721 ATCATCATCGTCTACACCCTGATGATCCTGCGGTCTCAAGAGCGTCCGGCGTCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGCTGGTCCTCGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGCTGGTCCTCGGTGGTGGTG 840

Qy    841 GCAGTTCTTCGTCTGCTGTGGGACTCCCATTCACATATTCATCCTGTGGTGAGGCTCTCGGGG 900
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Db    841 GCAGTTCTTCGTCTGCTGTGGGACTCCCATTCACATATTCATCCTGTGGTGAGGCTCTCGGGG 900

Qy    901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
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Db    961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTC 1080
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Db   1021 TTCCGGGACTTCTGCTTCCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154
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RESULT 2
ADN30505
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ID   ADN30505 standard; cDNA; 1154 BP.
XX
AC   ADN30505;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, wild-type cDNA.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol ; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
OS   chromosome 8q11.2.
OS   Homo sapiens.
XX
FH   Key                Location/Qualifiers
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FT                      replace(843,G)
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FT   variation          /standard_name= "Single nucleotide polymorphism"
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PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PR   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Claim 1; SEQ ID NO 1; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful for
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one addictive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the most common, wild-type allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match             99.9%;  Score 1152.4;  DB 12;  Length 1154;
Best Local Similarity   99.9%;  Pred. No. 6.7e-273;
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Matches 1153;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCGGGAGCCCGGGCCCCTGCGCCCGAGCGCC   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCGGGAGCCCGGGCCCCTGCGCCCGAGCGCC   60

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGCGCTGGGCCGAGCAGCAGCAACGGC      120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGCGCTGGGCCGAGCAGCAGCAACGGC      120

Qy  121 AGGCCGGCCTCGGAGGACGCGCAGCTGAGACCCCGCCACATCTCCCCGGCCATCCCGGTC     180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGGCCGGCCTCGGAGGACGCGCAGCTGAGACCCCGCCACATCTCCCCGGCCATCCCGGTC     180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTCGGCGTTGGTGGGGTTGGTGGCAACTCGCTGGTC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTCGGCGTTGGTGGGGTTGGTGGCAACTCGCTGGTC  240

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC   300

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATACGGGTCTACTTG     360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATACGGGTCTACTTG     360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCGCTACATTGCCGTG   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCGCTACATTGCCGTG   480

Qy  481 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC     540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC     540

Qy  541 TGCATCTGGCTGCTGTCGTCATCGTGTGCAATAGTCCTTGGAGGCACCAA            600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTCATCGTGTGCAATAGTCCTTGGAGGCACCAA            600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC    660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC    660

Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC   720

Qy  721 ATCATCATCGTCTACACACCTGATGATCCTGATCCGGTCTCAAGAGCGTCCGGTCCTCTTTCT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTACACACCTGATGATCCTGATCCGGTCTCAAGAGCGTCCGGTCCTCTTTCT  780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG      840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG      840

Qy  841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCACATATTCTTCAAGCGGTCTCGGGG    900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCACATATTCTTCAAGCGGTCTCGGGG    900

Qy  901 AGCACCTCCCAGCACAGCAGCTGCTCCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGCACCTCCCAGCACAGCAGCTGCTCCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT   960

Qy  961 ACCAACAGTAGCCTGAATCCCATTTCTTCTTCGATGAAAACTTCAAGCGGTGT         1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAACAGTAGCCTGAATCCCATTTCTTCTTCGATGAAAACTTCAAGCGGTGT         1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
```

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Qy        1 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60

Db

Qy       61 TGCCTGCCCCCACAGCAGCGCGCCGGCTGGTTCCCGCCTGGCGGGCTGGGCCGAGCCGCAGCCGCAGCGGC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTGCCCCCACAGCAGCGCGCCGGCTGGTTCCCGCCTGGCGGGCTGGGCCGAGCCGCAGCCGCAACGGC  120

Qy      121 AGCGCCGGCTCGGAGGACCGCGCAGCTGGACCTGGAGCCCGGCCGCCGCACATCTCCCGGCCCATCCCGGTC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCGCCGGCTCGGAGGACCGCGCAGCTGGACCTGGAGCCCGGCCGCCGCCGCACATCTCCCGGCCCATCCCGGTC  180

Qy      181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTCGTGTC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTCGTGTC  240

Qy      241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC  300

Qy      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy      361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420

Qy      421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy      541 TGCATCTGGCTGCTGTCTGTCATCTGTTGGCATCTCTGGAGTGCTCCTGCAGTGCCACCAAA  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGCATCTGGCTGCTGTCTGTCATCTGTTGGCATCTCTGGAGTGCTCCTGCAGTGCCACCAAA  600

Qy      601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC  660

Qy      661 TGGTGGGACCCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGGTGGGACCCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720

Qy      721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy      781 GGCTCCCGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGCGTAGGATCACCAGACTGTCCTGGTGGTGGTG  840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTCCCGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGCGTAGGATCACCAGACTGTCCTGGTGGTGGTG  840

Qy      841 GCAGTCTTCGTCGTCTGCTGCTGGACTCCCATTCACATATTCACATATTCCTCGTGAGGCTCTGGGG  900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCAGTCTTCGTCGTCTGCTGCTGGACTCCCATTCACATATTCACATATTCCTCGTGAGGCTCTGGGG  900

Qy      901 AGCACCTCCACAGCACAGTCTGCTCTCTCCCAGCTATTCTTCGCATTGCCTAGGCTAT  960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AGCACCTCCACAGCACAGTCTGCTCTCTCCCAGCTATTCTTCGCATTGCCTAGGCTAT  960

Qy      961 ACCAACAGTAGCCTGAATCCCATTCCTTCTTGATGAAAACTTCAAGCGGTGT  1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACAGTAGCCTGAATCCCATTCCTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy     1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080

Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
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Qy     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
            |||||||||||||||
Db     1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy     1141 TGACTAGTCGTGGA  1154
            ||||||||||||||
Db     1141 TGACTAGTCGTGGA  1154
```

RESULT 3
ADR44858

ID   ADR44858 standard; cDNA; 1154 BP.
XX
AC   ADR44858;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human kappa opioid receptor encoding cDNA SEQ ID NO:30.
XX
KW   opioid receptor; nerve cell; analgesic; gene therapy; pain; human;
KW   kappa opioid receptor; chromosome 8; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1143
FT   /*tag= a
FT   /product= "kappa opioid receptor"
XX
PN   WO2004073646-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-US004914.
XX
PR   19-FEB-2003; 2003US-0448663P.
XX
PA   (UYRP) UNIV ROCHESTER.
XX
PI   Kyrkanides S, Tallents RH;
XX
DR   WPI; 2004-635472/61.
DR   P-PSDB; ADR44857.
DR   GENBANK; U17298.
XX
PT   New vector for delivering an opioid receptor to a nerve cell comprising a
PT   sequence encoding a mu-opioid receptor and a vector backbone, useful in
PT   preparing a composition for reducing pain.
XX
PS   Disclosure; SEQ ID NO 30; 147pp; English.
XX
CC   The present invention describes a vector for delivering an opioid
CC   receptor to a nerve cell. The method comprises a sequence encoding an
CC   opioid receptor and a vector backbone. Also described: (1) a cell
CC   comprising the vector or its integrated product; (2) an animal comprising
CC   the cell; (3) reducing pain in a subject; (4) producing the vector; (5)
CC   producing the cell; and (6) an animal produced by the process of
CC   administering the vector to the animal. The vector has analgesic
CC   activity, and can be used in gene therapy. The vector is useful in
CC   preparing a composition for reducing pain in a subject. The present
CC   sequence encodes the human kappa opioid receptor, which is used in the
CC   exemplification of the present invention. The human kappa opioid receptor
CC   gene is located on chromosome 8, more specifically to 8q11-12.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match   99.9%; Score 1152.4; DB 13; Length 1154;
Best Local Similarity   99.9%; Pred. No. 6.7e-273;
Matches 1153; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

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Qy        1 ATGGACTCCCGATCCAGATCTTCCGGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1141 TGACTAGTCGTGGA 1154
             |||||||||||||
Db      1141 TGACTAGTCGTGGA 1154

RESULT 4
ADN30506
ID   ADN30506 standard; cDNA; 1154 BP.
XX
AC   ADN30506;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C852T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          replace(852,C)
FT                   /*tag= a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 2; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release,
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C852T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match          99.7%;  Score 1150.8; DB 12;  Length 1154;
Best Local Similarity  99.8%;  Pred. No. 1.7e-272;
Matches 1152; Conservative   0; Mismatches   2;  Indels    0;  Gaps    0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCGGGCCTACCTGCGCCCCCGAGCGGCCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCGGGCCTACCTGCGCCCCCGAGCGGCCC 60

Qy    61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTCCCGCTGGGCCGAGCCGAGCAGCAGCAACGGC 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTCCCGCTGGGCCGAGCCGAGCAGCAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGGCAGCTGAGCCCGCGACATCTCCCGGCCATCCCGGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGGCAGCTGAGCCCGCGACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGCAACTCGCTGGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCTTTCAGAGTACGGTCACTTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCTTTCAGAGTACGGTCACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTCACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTCACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCGTGCTCATCGTGTGGCATCTTCTGCAATAGTCCTTGGAGGCACCAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCGTGCTCATCGTGTGGCATCTTCTGCAATAGTCCTTGGAGGCACCAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCCAGTCCCAGATGATGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCCAGTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGCCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATCGTCGTCTACACCCTGATGATCCTGCGTCCACAAGAGCGTCCGGTCCTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCGTCTACACCCTGATGATCCTGCGTCCTCAAGAGCGTCCGGTCCTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
```

The invention relates to an isolated variant allele of a human kappa
opioid receptor gene, comprising a DNA sequence having at least one
variation in a fully defined wild-type allele of human kappa opioid
receptor (hKOR) sequence appearing as ADN30505, where the variation
comprises C852T, C948T, C1008T or their combinations. Also included are
an isolated nucleic acid molecule selectively hybridising to the variant,
a cloning vector comprising the variant and an origin of replication, an
expression vector comprising the variant associated with a promoter, a
unicellular host transformed/transfected with the vector and a commercial
test kit for determining the presence of at least one variation in a hKOR
gene of an allele in a bodily sample taken from a subject. The hKOR
variant allele is useful for determining a susceptibility in a subject to
at least one physiological response, condition or disease related to the
endogenous opioid system, nociception, neurotransmitter release
endogenous opioid system, learning, memory, cognition, pain, cocaine,
amphetamine and other stimulants self-administration, behavioural
sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
amphetamine and alcohol withdrawal, physical dependence and tolerance,
neuroendocrine function, reproductive function, prolactin regulation,
stress responsivity, physiology and pathology of mood and affect, immune
function, gastrointestinal function. The hKOR variant allele is useful for
determining a susceptibility to pain in a subject and is useful for
determining a therapeutically effective amount of pain reliever to
administer to a subject in order to induce analgesia in the subject. The
hKOR variant allele is useful for determining a therapeutically effective
amount of therapeutic agent to administer to a subject suffering from at
least one addictive disease to treat the at least one addictive disease.
The gene for hKOR is located on chromosome 8q11.2. The present sequence
is the A843G allele of hKOR.

```
Qy   841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCATCCTGGTCGAGGCTCTGGGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCATCCTGGTCGAGGCTCTGGGG 900

Qy   901 AGCACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT 1020

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTC 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy  1141 TGACTAGTCGTGGA 1154
             ||||||||||||||
Db  1141 TGACTAGTCGTGGA 1154
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RESULT 5
ADN30510
ID   ADN30510 standard; cDNA; 1154 BP.
XX
AC   ADN30510;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, A843G allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   allele   replace(843,A)
FT   /*tag= a
FT   /standard_name= "single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 6; 29pp; English.
XX

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity   99.8%; Pred. No. 1.7e-272;
Matches 1152;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

SQ   Sequence 1154 BP; 238 A; 339 C; 288 G; 289 T; 0 U; 0 Other;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCGGCCGCCGGCCTACCTGCGGCCCCGAGCGGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCGGCCGCCGGCCTACCTGCGGCCCCGAGCGGCC 60

Qy    61 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAACGGC 120

Qy   121 AGCGGCCGGCTCGGAGGACGCGGCAGCTGGAGCCGCCGCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCCGGCTCGGAGGACGCGGCAGCTGGAGCCGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGTGGCCAACTCGCTGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGTGGCCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCATGCCCTTTCAGAGTACATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCATGCCCTTTCAGAGTACATTTAAC 300

Qy   301 CTGGCTTGGCAGATGCTTTAGTTACTACACAAGATGCTGTGCAAGATGATGAGCGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTGGCAGATGCTTTAGTTACTACACAAGATGCTGTGCAAGATGATGAGCGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCTACACTTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Db 541 TGCATCTGGCTGCTGCGTCGTCATCGTGGCATCCTGCGATGACTACTCC 600
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Qy 601 GTCAGGGAAGAGCTGCGATGTCATTGAGTGCTCCTGCGAGTTCCCAGATGACTACTCC 660
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Db 601 GTCGGGGAAGAGCTGCGATGTCATTGAGTGCTCCTGCGAGTTCCCAGATGACTACTCC 660

Qy 661 TGGTGGGACCTTCTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
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Db 661 TGGTGGGACCTTCTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy 721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTCGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTCGTG 840

Qy 841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
         || ||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GCGGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
         |||||||||||||||||||||||||| |||||||||||||||||||||||
Db 901 AGCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy 961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
         ||||||||||||| ||||| |||||||| ||| |||||||||||||||||
Db 961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTC 1080
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Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGACGGACATCGATGGGATGAATAAACCAGTA 1140
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Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGACGGACATCGATGGGATGAATAAACCAGTA 1140

Qy 1141 TGACTAGTCGTGGA 1154
         ||||||||||||||
Db 1141 TGACTAGTCGTGGA 1154

RESULT 6
ADN30508
ID ADN30508 standard; cDNA; 1154 BP.
XX
AC ADN30508;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human kappa opioid receptor, hKOR, C1008T allele.
XX
KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW single nucleotide polymorphism; endogenous opioid system; nociception;
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW amphetamine; alcohol; tobacco; opiate; withdrawal;
KW neuroendocrine function; reproductive function; prolactin regulation;
KW stress responsivity.; mood; affect; immune function;
KW gastrointestinal function; analgesia; additive disease;
KW chromosome 8q11.2.
XX
OS Homo sapiens.
XX
FH   Location/Qualifiers
FT allele   replace(1008,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN US2004097704-A1.
XX
PD 20-MAY-2004.

XX
PF 13-JUL-2001; 2001US-00904584.
XX
PR 14-JUL-2000; 2000US-0218300P.
XX
PA (KREE/) KREEK M J.
PA (YUFE/) YUFEROV V.
PA (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, Yuferov V, Laforge KS;
XX
DR WPI; 2004-389204/36.
XX
PT Novel isolated variant allele of human kappa opioid receptor gene, useful
PT for determining susceptibility in subject to physiological response,
PT condition or disease related to endogenous opioid system.
XX
PS Example; SEQ ID NO 4; 29pp; English.
XX
CC The invention relates to an isolated variant allele of a human kappa
CC opioid receptor gene, comprising a DNA sequence having at least one
CC variation in a fully defined wild-type allele of human kappa opioid
CC receptor (hKOR) sequence appearing as ADN30505, where the variation
CC comprises C852T, C948T, C1008T or their combinations. Also included are
CC an isolated nucleic acid molecule selectively hybridising to the variant,
CC a cloning vector comprising the variant and an origin of replication, an
CC expression vector comprising the variant associated with a promoter, a
CC unicellular host transformed/transfected with the vector and a commercial
CC test kit for determining the presence of at least one variation in a hKOR
CC gene of an allele in a bodily sample taken from a subject. The hKOR
CC variant allele is useful for determining a susceptibility in a subject to
CC at least one physiological response, condition or disease related to the
CC endogenous opioid system, nociception, neurotransmitter release
CC endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC amphetamine and other stimulants self-administration, behavioural
CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC amphetamine and alcohol, withdrawal, physical dependence and tolerance;
CC neuroendocrine function, reproductive function, prolactin regulation,
CC stress responsivity, physiology and pathology of mood and affect, immune
CC function, gastrointestinal function. The hKOR variant allele is useful
CC for determining a susceptibility to pain in a subject and is useful for
CC determining a therapeutically effective amount of pain reliever to
CC administer to a subject in order to induce analgesia in the subject. The
CC hKOR variant allele is useful for determining a therapeutically effective
CC amount of therapeutic agent to administer to a subject suffering from at
CC least one addictive disease to treat the at least one additive disease.
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC is the C1008T allele of hKOR.
XX
SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity   99.8%; Pred. No. 1.7e-272;
Matches 1152 Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy 1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCGCCTACCTGCTGCCCGCCAGCGCC 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCGCCTACCTGCTGCCCGCCAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGGTGGCCGGCACCAGCAGCAGCAACGGC 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGGTGGCCGGCACCAGCAGCAGCAACGGC 120

Qy 121 AGCGCCGGCTCGGAGGACGGCGGCAGCTGGAGCCTGCAGCATCTCCCGGGTC 180
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Db 121 AGCGCCGGCTCGGAGGACGGCGGCAGCTGGAGCCTGCAGCATCTCCCGGGTC 180

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATTTACC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||

KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW single nucleotide polymorphism; endogenous opioid system; nociception;
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW amphetamine; alcohol; tobacco; opiate; withdrawal;
KW neuroendocrine function; reproductive function; prolactin regulation;
KW stress responsivity.; mood; affect; immune function;
KW gastrointestinal function; analgesia; additive disease;
XX
OS Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT allele   replace(846,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN US2004097704-A1.
XX
PD 20-MAY-2004.
XX
PF 13-JUL-2001; 2001US-00904584.
XX
PR 14-JUL-2000; 2000US-0218300P.
XX
PA (KREE/) KREEK M J.
PA (YUFE/) YUFEROV V.
PA (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, Yuferov V, Laforge KS;
XX
DR WPI; 2004-389204/36.
XX
PT Novel isolated variant allele of human kappa opioid receptor gene, useful
PT for determining susceptibility in subject to physiological response,
PT condition or disease related to endogenous opioid system.
XX
PS Example; SEQ ID NO 7; 29pp; English.
XX
CC The invention relates to an isolated variant allele of a human kappa
CC opioid receptor gene, comprising a DNA sequence having at least one
CC variation in a fully defined wild-type allele of human kappa opioid
CC receptor (hKOR) sequence appearing as ADN30505, where the variation
CC comprises C852T, C948T, C108T or their combinations. Also included are
CC an isolated nucleic acid molecule selectively hybridising to the variant,
CC a cloning vector comprising the variant and an origin of replication, an
CC expression vector comprising the variant associated with a promoter, a
CC unicellular host transformed/transfected with the vector and a commercial
CC test kit for determining the presence of at least one variation in a hKOR
CC gene of an allele in a bodily sample taken from a subject. The hKOR
CC variant allele is useful for determining a susceptibility in a subject to
CC at least one physiological response, condition or disease related to the
CC endogenous opioid system, nociception, neurotransmitter release
CC endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC amphetamine and other stimulants self-administration, behavioural
CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC neuroendocrine function, reproductive function, prolactin regulation,
CC stress responsivity, physiology and pathology of mood and affect, immune
CC function, gastrointestinal function. The hKOR variant allele is useful for
CC determining a susceptibility to pain in a subject and is useful for
CC determining a therapeutically effective amount of pain reliever to
CC administer to a subject in order to induce analgesia in the subject. The
CC hKOR variant allele is useful for determining a therapeutically effective
CC amount of therapeutic agent to administer to a subject suffering from at
CC least one addictive disease to treat the at least one additive disease.
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC is the C846T allele of hKOR.
XX
SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Db Human; kappa opioid receptor; hKOR; ss; gene; SNP;

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Qy  241 ATGTTCGTGATCATCCGATACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTAGTTACTACTACAACAACCCCTTTCAGAGTACGGTCTACTTG 360
Qy  301 CTGGCTTTGGCAGATGCTTAGTTACTACTACAACAACCCCTTTCAGAGTACGGTCTACTTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
Qy  541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
Qy  601 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGTCCTCGTCTCC 720
Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGTCCTCGTCTCC 720
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Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATGCAACCTGCGTAGGATCACCAGACTGGTCCTTGGTGTGGTG 840
Qy  781 GGCTCCCGAGAGAAAGATGCAACCTGCGTAGGATCACCAGACTGGTCCTTGGTGTGGTG 840
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Db  841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCATCCTGGTGAGGCGTCCTGGGG 900
Qy  841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCATCCTGGTGAGGCGTCCTGGGG 900
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Qy  901 AGCACCTCCACAGCACAGCGTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
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Db  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
Qy  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTCAAGCGGTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGGATGGAGCGCAGAGCACTAGCAGAGTC 1080
Qy 1021 TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGGATGGAGCGCAGAGCACTAGCAGAGTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCCGATGGGAATAAAACCAGTA 1140
Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCCGATGGGAATAAAACCAGTA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1141 TGACTAGTCGTGGA 1154
            ||||||||||||||
Db 1141 TGACTAGTCGTGGA 1154
```

RESULT 7
ADN30511
ID ADN30511 standard; cDNA; 1154 BP.
XX
AC ADN30511;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human kappa opioid receptor, hKOR, C856T allele.
XX

Query Match   99.7%;   Score 1150.8;   DB 12;   Length 1154;
Best Local Similarity 99.8%;   Pred. No. 1.7e-272;
Matches 1152;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCGCCCCGAGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCGCCCCGAGCGCC 60

Qy   61 TGGCTGCCCCAACAGCAGCAGCGGCGCTGGTTCCCGGCCGCAGCCCGACAGCAACGGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGGCTGCCCCAACAGCAGCAGCGGCGCTGGTTCCCGGCTGGCCAGCCCGACAGCAACGGC 120

Qy 121 AGGCGCCGGCTCGGAGGACGCGCGAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGGCGCCGGCTCGGAGGACGCGCGAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy 241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGTTCGTGATCATCCGATACACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy 301 CTGGCCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CTGGCCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGGTACATTGCCGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGGTACATTGCCGTG 480

Qy 481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCATAATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTGTCGTCGTCATCTCGTTGGCATCTCGTTGGCATGTCCTTGGGAGGCACCAAA 600
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Db 541 TGCATCTGGCTGCTGTCGTCGTCATCTCGTTGGCATCTCGTTGGCATGTCCTTGGGAGGCACCAAA 600

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
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Db 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTGGATCCCGTCCTC 720

Qy 721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTG 840

Qy 841 GCAGTCTTCGTCGTCTGCTGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GCAGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACCTTCCACAGCACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 AGCACCTTCCACAGCACAGCAGTCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy 961 ACCAAAGTAGCCTGAATCCAGGCCTTTCTTGATGAAAACTTCAAGCGTGT 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 ACCAAAGTAGCCTGAATCCCATTCCATTCACGGCCTTTCTTGATGAAAACTTCAAGCGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGCGGCAGAGCGGCACTAGCAGAGTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGCGGCAGAGCGGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGATGAATAAACCAGTA 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGATGAATAAACCAGTA 1140

Qy 1141 TGACTAGTCGTGGA 1154
        ||||||||||||||
Db 1141 TGACTAGTCGTGGA 1154

RESULT 8
ADN30509
ID   ADN30509 standard; cDNA; 1154 BP.
XX
AC   ADN30509;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, G36T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   allele   replace(36,G)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 5; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural

```
CC    sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC    amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC    neuroendocrine function, reproductive function, prolactin regulation,
CC    stress responsivity, physiology and pathology of mood and affect, immune
CC    function, gastrointestinal function. The hKOR variant allele is useful
CC    for determining a susceptibility to pain in a subject and is useful for
CC    determining a therapeutically effective amount of pain reliever to
CC    administer to a subject in order to induce analgesia in the subject. The
CC    hKOR variant allele is useful for determining a therapeutically effective
CC    amount of therapeutic agent to administer to a subject suffering from at
CC    least one addictive disease to treat the at least one addictive disease.
CC    The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC    is the G36T allele of hKOR.
XX
SQ    Sequence 1154 BP; 239 A; 339 C; 286 G; 290 T; 0 U; 0 Other;

Query Match        99.7%;  Score 1150.8; DB 12;  Length 1154;
Best Local Similarity  99.8%;  Pred. No. 1.7e-272;
Matches 1152;  Conservative   0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCTACCTGCGCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCTACCTGCGCCCGAGCGCC 60

Qy     61 TGCCTGCCCCAACAGCAGCAGCCGCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACCGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCAACAGCAGCAGCCGCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACCGC 120

Qy    121 AGGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGCGCCACATCTCCCGCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGCGCCACATCTCCCGCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTTGGTCGGCAACTCGCTGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTTGGTCGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGACAAAGATTTACATATTTAACAT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGACAAAGATTTACATATTTAACAT 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCCTCATCGTGTGGCATCTCTGGAGGCACCAAA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCCTCATCGTGTGGCATCTCTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTCGATGCTCATTGAGTGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGCTCATTGAGTGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGGACCTCTTCATGGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGCTCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGGACCTCTTCATGGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGCTCTC 720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCAACCTGCCTGGTGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCAACCTGCCTGGTGTGGTG 840

Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGCGTGGAGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGCGTGGAGGCTCTGGGG 900

Qy    901 AGCACCTCCCACAGCACAGTCTCTCCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCACAGCACAGTCTCTCCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCTGTTCTTCTTGATGAAAACTTCAAGCGCGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCCTGTTCTTCTTGATGAAAACTTCAAGCGCGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAACAGTAGACAGAGCGCGCAGAGCACTAGCACGAGTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAACAGTAGACAGAGCGCGCAGAGCACTAGCACGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATTCGATGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATTCGATGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154
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RESULT 9
AB242678
```
ID   AB242678 standard; DNA; 1182 BP.
XX
AC   AB242678;
XX
DT   04-MAR-2003 (first entry)
XX
DE   Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,   Roush CL,   Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81832.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
```

XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match   99.2%; Score 1144.4; DB 8; Length 1182;
Best Local Similarity   99.5%;   Pred. No. 6.2e-271;
Matches 1148;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCTCCCGGGAGGCCCCCGAGCGCGC 60
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGGCCTCCCGGGAGGCCCCCGAGCGCGC 73

Qy   61 TGCCTGCCCCCCAACAGCAGCCGCTGGTTTCCCGGTGGGCGGCCGAGCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCCAACAGCAGCCGCTGGTTTCCCGGTGGGCGGCCGAGCCGACAGCAACGGC 133

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCTGGAGCCGGCCATCTCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCGCACATCTCTCCCCGGCCGCCATCTCCCGGTC 193

Qy   181 ATCATCACGGCGGGGTCACTCCGTAGTGTTCGTGCGCCATGATGAGCCGAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGGGTCACTCCGTAGTGTTCGTGCGCCATGATGAGCCGAACTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGACAGCAACCAACATTACATATTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGACAGCAACCAACATTACATATTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGATACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGATACGGTCTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGATCTTCACCTTGACCATGATGAGCCGTGGACCGGTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCGTCGTCATCGTGTTGGCATCTCTCGCAATAGTCCTTGAGGCCACCAAA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCGTCGTCATCGTGTTGGCATCTCTCTGCAATAGTCCTTGAGGCCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCCAGTTCCCAGATGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCTTGCCTCGTGATCCCGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTCGTGATCCCGTCCTC 733

Qy   721 ATCATCATCGTCTGCTACACCCTGCGTCTCAAGAGCCTCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCCTCCGGCTCCTTTCT 793

Qy   781 GGCTCCCGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCGTCGGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCGTCGGTGGTG 853

Qy   841 GCAGTCTCTGTCGTCGTGGACTCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCCGGTTTCGTGTCGTGGACTCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG 913

Qy   901 AGCACCTCCCAGCACAGCTGCTCTCCAGCTATTACTTTCTGCATTGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTTACTTGCATCGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCCGGGACTTTCTGTTTCCACTGAAGATGAAGATGAGGAGGCGGCAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCTGCTTGTTTCCACTGAAGATGAGGATGAGGAGGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGA 1154
           |||||||||||||
Db   1154 TGACTAGTCGTGA 1167

RESULT 10
AAD58490
ID   AAD58490 standard; DNA; 1182 BP.
XX
AC   AAD58490;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human kappa opioid receptor 1 (KOR) DNA.
XX
KW   Human; urological disorder; urinary incontinence; gene therapy; cancer;
KW   kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
KW   urethra; overflow urinary incontinence; stress urinary incontinence;
KW   nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
KW   kappa opioid receptor 1; KOR; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT
FT   CDS   14..1156
FT   /tag= a
FT   /product= "Human kappa opioid receptor 1 (KOR)"
FT   /note="The CDS is referred to as SEQ ID NO:21 in the
FT   specification"
XX
PN   WO2003061573-A2.
XX
PD   31-JUL-2003.
XX
PF   16-JAN-2003; 2003WO-US001450.
XX
PR   18-JAN-2002; 2002US-0349511P.

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PR   28-FEB-2002; 2002US-0360500P.
PR   15-MAR-2002; 2002US-0365041P.
PR   19-APR-2002; 2002US-0374063P.
PR   14-AUG-2002; 2002US-0403468P.
PR   27-SEP-2002; 2002US-0414262P.
PR   21-OCT-2002; 2002US-0419986P.
PR   05-NOV-2002; 2002US-0423809P.
PR   26-NOV-2002; 2002US-0429797P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Silos-Santiago I, Karicheti V;
XX
DR   WPI; 2003-598705/56.
DR   P-PSDB; AAE38589.
XX
PT   Identifying a compound for treating urological disorders, for example
PT   urinary incontinence by assaying the ability of the compound to modulate
PT   the nucleic acid expression or polypeptide activity.
XX
PS   Disclosure; Page 149-151; 0pp; English.
XX
CC   The present relates to a method for identifying a compound for treating
CC   urological disorders e.g., urinary incontinence including overactive/
CC   oversensitive bladder, overflow urinary incontinence, stress urinary
CC   incontinence caused by dysfunction of the bladder, urethra or central or
CC   peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC   cancer of the prostate or kidney disorders. The method is also useful for
CC   modulating hyperplasia in a cell and treating a subject having a
CC   urological disorder. The invention is also used in gene therapy. The
CC   present sequence is human kappa opioid receptor 1 (KOR) DNA
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match        99.2%;  Score 1144.4;  DB 10;  Length 1182;
Best Local Similarity 99.5%;  Pred. No. 6.2e-271;
Matches 1148;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy       1 ATGGACTCCCGATCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCTGGCCCTACCTGCGCCCCGAGCGGC 73

Qy      61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCGGCCGGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 TGCCTGCCCCCAACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCGGCCGGACAGCAACGGC 133

Qy     121 AGCGGCCGGCTCGGAGGACGCGCAGCGCGGCAGCTGGAGCTCCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 AGCGGCCGGCTCGGAGGACGCGCAGCGCGGCAGCTGGAGCTCCCCGGCCATCCCGGTC 193

Qy     181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy     301 CTGGCCTTTGGCAGATGCTTTAGTTACTACAACAACATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 CTGGCCTTTGGCAGATGCTTTAGTTACTACAACAACATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy     361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493

Qy     481 TGCCACCCCGTGAAGGCTTTGACTTCCGACACCCTTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553
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Qy     541 TGCATCTGGCTGCTGTCGTCATCTCTGCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     554 TGCATCTGGCTGCTGTCGTCGTCATCTCTGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy     601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCGTCTCCTTCCAGATGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCGTCTCCTTCCAGATGATGACTACTCC 673

Qy     661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTCGTCGTGATCCCTGTCTC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTCATCTTGTCGTGATCCCTGTCTC 733

Qy     721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCGTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     734 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCGTCCTTTCT 793

Qy     781 GGCTTCCCAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     794 GGCTTCCCAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy     841 GCAGTCTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCCTGGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     854 GCGGTTTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCCTGGGGG 913

Qy     901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGTATTACTTCTGCATTGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     914 AGCACCTCCACAGCACAGCTGCTCTCTCCAGTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy     961 ACCAACAGTAGCTTGAATCCCATTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1033

Qy    1021 TTCCGGGACTTCTGCTTCCACTGAAGATGGAGGATGGAGGCGGCAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1034 TTCCGGGACTTCTGCTTCTCGCTTTCCACTGAAGATGGAGGATGGAGGCGGCAGAGCACTAGCAGAGTC 1093

Qy    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATGAAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATGAAAACCAGTA 1153

Qy    1141 TGACTAGTCGTGGA 1154
           |||||||||||||
Db    1154 TGACTAGTCGTGGA 1167
```

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RESULT 11
ADE84861
ID   ADE84861 standard; DNA; 1182 BP.
XX
AC   ADE84861;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Farnesyl transferase inhibitor modulated leukemia associated gene #80.
XX
KW   ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW   quinolinone; leukemia; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003038129-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US034784.
XX
PR   30-OCT-2001; 2001US-0338997P.
PR   30-OCT-2001; 2001US-0340081P.
PR   30-OCT-2001; 2001US-0340938P.
PR   30-OCT-2001; 2001US-0341012P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
```

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XX
PI   Raponi M;
XX
DR   WPI; 2003-513497/48.
XX
PT   Determining whether a patient will respond to treatment with a farnesyl
PT   transferase inhibitor, by analyzing the expression of gene that is
PT   differentially modulated in the presence of the inhibitor.
XX
PS   Disclosure; SEQ ID NO 80; 346pp; English.
XX
CC   The invention relates to a method of determining whether a patient will
CC   respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC   analyzing the expression of gene that is differentially modulated in the
CC   presence of an FTI. The method is useful for determining whether a
CC   patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC   chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl-4-(3-chlorophenyl)-1-
CC   methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC   patient with leukaemia with FTI if the analysis indicates that the patient
CC   will respond. This sequence corresponds to a gene whose expression may be
CC   modulated in the presence of FTI.
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match            99.2%;   Score 1144.4;   DB 10;   Length 1182;
Best Local Similarity  99.5%;   Pred. No. 6.2e-271;
Matches 1148;   Conservative  0;   Mismatches  6;   Indels  0;   Gaps  0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCCCCGAGCGCC     60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCTGGCCCTACCTGCGCCCGAGCGCC    73

Qy    61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGAGCCCGACAGCAACGGC    120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCTGGGAGCCCGACAGCAACGGC    133

Qy   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGGCACATCTCCCCGGCCATCCCCGGTC    180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGGCACATCTCCCCGGCCATCCCCGGTC    193

Qy   181 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC    240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC    253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTTACATATTTAAC    300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTTACATATTTAAC    313

Qy   301 CTGGCTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATGACGGTCTACTTG    360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATGACGGTCTACTTG    373

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC    433

Qy   421 AACATGTTCACCAGCATCTTCACCTTCACCTTCACCCTACACATTGCCGTG    480
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTCACCTTCACCCTACACATTGCCGTG    493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCGAAGGCAAAGATCATCAATATC    540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCGAAGGCAAAGATCATCAATATC    553

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA    600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAA    613

Qy   601 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC    660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC    673

Qy   661 TGGTGGGGACCTTCTTCATGAAGATCGTGCTCTTCATCTTTGCCTTCGTGTGATCCCGTCCTC    720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGGACCTTCTTCATGAAGATCGTGCTCTTCATCTTTGCCTTCGTGTGATCCCGTCCTC    733

Qy   721 ATCATCATCGTCTGCTACACCCTGCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT    780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACACCCTGCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT    793

Qy   781 GGCTCCCGAGAGAAAGATGCGAACCTGCTAGGATCACCAGACTGGTCCTGGTGTGGGTG    840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAAGATGCGAACCTGCTAGGATCACCAGACTGGTCCTGGTGTGGGTG    853

Qy   841 GCAGTCTTCGTGCTGCTGGACTCCCATTGACATATTCACTCGGTGGAGGCTCTGGGG    900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTGCTGGACTCCCATTCACATATTCACATATCCTGGTGGAGGCTCTGGGG    913

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT    960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT    973

Qy   961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT   1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT   1033

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGGCAGAGCACTAGCAGAGTC   1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGGCAGAGCACTAGCAGAGTC   1093

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA   1153

Qy  1141 TGACTAGTCGTGGA   1154
         ||||||||||||||
Db  1154 TGACTAGTCGTGGA   1167


RESULT 12
ACA56819
ID   ACA56819 standard; cDNA; 1182 BP.
XX
AC   ACA56819;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1417.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
PF   30-JAN-1998;   98US-00016434.
XX
PR   30-JAN-1998;   98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J,   Seilhamer JJ;
XX
DR   WPI; 2003-352189/33.
XX
PT   Combination of polynucleotide probes, useful as array elements in a
PT   microarray for monitoring the expression of a number of target
PT   polynucleotides.
XX
PS   Claim 1; SEQ ID NO 1417; 65pp; English.
XX
CC   The invention relates to a combination which, comprises a number of
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CC   polynucleotide probes comprising a sequence selected from one of the 1490
CC   sequences mentioned in the specification. The combination is useful as an
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

  Query Match            99.2%;  Score 1144.4;  DB 10;  Length 1182;
  Best Local Similarity  99.5%;  Pred. No. 6.2e-271;
  Matches 1148;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
              ||||| |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db         14 ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCTGGCCCTACCTGCGCCCCGAGCGCC 73

Qy         61 TGCCTGCCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 TGCCTGCCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 133

Qy        121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 193

Qy        181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy        241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy        421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493

Qy        481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy        541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy        601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy        661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 733

Qy        721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy        781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy        841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 913

Qy        901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy        961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy       1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1093

Qy       1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy       1141 TGACTAGTCGTGGA 1154
              ||||||||||||||
Db       1154 TGACTAGTCGTGGA 1167

RESULT 13
ADI56615
ID   ADI56615 standard; DNA; 1182 BP.
XX
AC   ADI56615;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human polynucleotide probe #1417.
XX
KW   Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW   effector-like polypeptide; cancer; immunopathology; neuropathology;
KW   drug development; toxicology; carcinogenicity;
KW   signalling pathway polypeptide; adrenal gland; bladder; bone;
KW   bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW   diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW   dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS   Homo sapiens.
XX
PN   US2004010136-A1.
XX
PD   15-JAN-2004.
XX
PF   26-NOV-2002; 2002US-00305720.
XX
PR   30-JAN-1998;   98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J,  Seilhamer JJ;
XX
DR   WPI; 2004-090520/09.
XX
PT   New composition comprising polynucleotide probes, useful as array
PT   elements in a microarray for monitoring the expression of target
PT   polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
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PT   fragments.
XX
PS   Claim 6; SEQ ID NO 1417; 73pp; English.
XX
CC   The invention relates to a composition of polynucleotide probes
CC   comprising first polynucleotide probes comprising at least a portion of a
CC   gene encoding a receptor-like polypeptide, second polynucleotide probes
CC   comprising at least a portion of a gene encoding a transducing
CC   polypeptide and third polynucleotide probes comprising at least a portion
CC   of a gene encoding an effector-like polypeptide. The probes of the
CC   composition are useful as array elements in a microarray for monitoring
CC   the expression of target polynucleotides. The microarray is useful in the
CC   diagnosis and treatment of cancer, an immunopathology or a
CC   neuropathology. It can also be used for drug discovery and development,
CC   toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC   Microarrays can also be used for monitoring the progression of diseases
CC   that may be associated with the altered expression of signalling pathway
CC   polypeptides. The composition can also be used to purify a subpopulation
CC   of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC   is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC   the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC   an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC   ulcerative colitis, or a neuropathology, e.g. amnesia,
CC   epilepsy, Alzheimer's disease or depression. This sequence represents a
CC   human polynucleotide probe of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match   99.2%; Score 1144.4; DB 12; Length 1182;
Best Local Similarity 99.5%;   Pred. No. 6.2e-271;
Matches 1148; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCGCCCCGAGCGC   60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCGCCCCGAGCGC   73

Qy   61 TGCCTGCCCCCCAACAGCAGCGGCCGCCTGGTTTCCGGCTGGGCCGAGCCGACAGCAACGGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCCAACAGCAGCGGCCGCCTGGTTTCCGGCTGGGCCGAGCCGACAGCAACGGC 133

Qy   121 AGCGGCCGGCTCGGAGGACGCGCAGCTGAGCCCGGCGCACATCCCCCGGCCATCCCGGTC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGGCCGGCTCGGAGGACGCGCAGCTGAGCCCGGCGCACATCTCCCCGGCCATCCCGGTC 193

Qy   181 ATCATCACGGCCGTCTACTCCCGTAGTGTCGTGGCTTGGTGGCAACTCGCTGGTC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCCGTCTACTCCCGTAGTGTCGTGGCTTGGTGGCAACTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGATACGGTCTACTTG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCTTTCAGATACGGTCTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGACATCTTCACCTTGACCGGCTACATTGCCGTG 480
             ||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGACATCTTCACCTTGACCGGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGTTGCAATAGTCCTTGGAGGCACCAAA
             |||||||||||||||||||||||||||||||||||||||||||||||

Db   554 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGTTGGCATCTCTGTTGGAGGCACCAAA 613

Qy   601 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTCCGTCAGTTCCCAGATGATGACTACTCC 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTGCGATGTCATTGAGTGCTCCGTCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACCTCTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTC 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 733

Qy   721 ATCATCACGTCTGCTACACACCTGATGATCCTGCGTCTCAAGACCGTCCGGTCCCTTCT 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCTCAAGACCGTCCGGTCCCTTCT 793

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCGTCTGGTGGTG 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy   841 GCAGTCTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTTCGTGCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 913

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATTGCATTGCTAGGCTAT 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATTGCATTGCTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTGATGAAAAACTTCAAGCGGTGT 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTGATGAAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCGCTTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCCAGAGCACTAGCAGAGTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCGCTTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCCAGAGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGA 1154
             ||||||||||||
Db   1154 TGACTAGTCGTGA 1167

RESULT 14
AAT90998
ID   AAT90998 standard; cDNA; 1143 BP.
XX
AC   AAT90998;
XX
DT   14-APR-1998   (first entry)
XX
DE   Human kappa opioid receptor cDNA.
XX
KW   Selective target cell activation; G protein-coupled receptor; RASSL;
KW   gene therapy; cell proliferation; kappa opioid receptor; human;
KW   transgenic animal; arrhythmia; bone disease; seizure;
KW   vascular contraction; disease model; ss.
XX
OS   Homo sapiens.
XX
PN   WO9735478-A1.
XX
PD   02-OCT-1997.
XX
PF   25-MAR-1997;   97WO-US005334.
XX
PR   26-MAR-1996;   96US-00622348.
XX
PA   (REGC) UNIV CALIFORNIA.
XX
PI   Conklin BR;
XX
DR   WPI; 1997-502739/46.

DR   P-PSDB; AAW30297.
XX
PT   Selective activation of target cell expressing modified G protein coupled
PT   receptor - allows control of cellular proliferation, especially for
PT   amplification of transfected cells in gene therapy.
XX
PS   Example 1; Page 74-76; 117pp; English.
XX
CC   This cDNA sequence comprises the coding region for human kappa opioid
CC   receptor (KOR, see AAW30297), a G protein-coupled receptor implicated in
CC   neurotransmission. A novel method for selectively activating a target
CC   cell (TC) comprises: (i) introducing into the cell a nucleic acid
CC   sequence (I) that expresses a G protein-coupled receptor (A) modified to
CC   be activated superiorly by a synthetic ligand (RASSL); and (ii) exposing
CC   the transfected cell to small synthetic molecules (B) that bind to and
CC   activate (A), inducing the G protein coupled cellular response associated
CC   with receptor activation. (A) has: (a) decreased binding affinity for a
CC   selected natural ligand of the native receptor, (b) binding affinity for
CC   (B), and (c) is activated by binding (B) sufficiently to produce the
CC   required cellular response. Also new are: (1) transgenic cells including
CC   heterologous (I) in the genome; (2) cellular implants comprising a TC
CC   transfected with (I); (3) isolated (I); and (4) transgenic non-human
CC   animals expressing (A). Activation of (A) results, in vitro or in vivo,
CC   in cellular proliferation, or secretion of a cellular product,
CC   particularly a heterologous therapeutic protein encoded by a second
CC   inserted nucleic acid sequence. Particularly it is used to expand the
CC   relatively few cells that are successfully transfected during cell
CC   therapy procedures. Other responses that can be regulated are cell
CC   migration and contraction, or pigment production. In transgenic animals,
CC   expression or stimulation of (A) is designed to develop cardiac
CC   arrhythmia, symptoms of bone disease, seizures, vascular contractions,
CC   dementia, neurodegeneration etc. for use as models of these diseases
CC   (claimed). The transgenic animals are also used for production of
CC   improved food products (e.g. increased calcium content in eggshells or
CC   altered fat/lean ratios) or to control fertility or induce labour. A
CC   RASSL derived from KOR, designated RASSL OR1 (see AAW30299), was
CC   generated by mutation of the KOR cDNA sequence
XX
SQ   Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match   98.9%; Score 1141.4; DB 2; Length 1143;
Best Local Similarity   99.9%;
Matches 1142; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCCGGCCCTACCTGCGCCCTGCGCCGCGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCCGGCCCTACCTGCGCCCTGCGCCGCGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGGGCGGCCAGCTGGAGCCCGCCGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGGGCGGCCAGCTGGAGCCCGCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTCGGCCTTGGTGGGCAACTCGCTGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTCGGCCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATGTCTGCTACACCCTGATCCTGGCTCTCAAGAGCGTCCGGCTCCTTTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACCCTGATCCTGGCTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTCGTGCTCCTGGTGGTGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTCGTGCTCCTGGTGGTGTG 840

Qy   841 GCAGTCTTCGTGCTCGGACTCCATTCACATATTCATCTCGTGGAGGCTCTCGGGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTGCTCGGACTCCCATTCACATATTCATCTCGTGGAGGCTCTCGGGG 900

Qy   901 AGCACCTCCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATGAATAAACCAGTA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGA 1143
            |||
Db   1141 TGA 1143

RESULT 15
AAT12550
ID   AAT12550 standard; cDNA; 1142 BP.
XX
AC   AAT12550;
XX
DT   03-SEP-1996 (first entry)
XX
DE   Human kappa opioid receptor cDNA.
XX
KW   Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW   neurology; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1142
FT   /*tag= a
FT   /product= "kappa_opioid_receptor"
FT   /note= "incomplete termination codon"
XX

PN   WO9601898-A1.
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995;   95WO-FR000912.
XX
PR   11-JUL-1994;   94FR-00008531.
XX
PA   (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX
PI   Kieffer B.- Simonin F;
XX
DR   WPI; 1996-097628/10.
DR   P-PSDB; AAR88722.
XX
PT   New nucleic acid encoding the human Kappa opioid receptor - useful in
PT   diagnosis and therapy, and for isolating receptor ligands and modulators.
XX
PS   Claim 3; Page 13-15; 30pp; French.
XX
CC   This sequence codes for the human kappa opioid receptor and was obtained
CC   from two overlapping cDNA fragments isolated from a human placental cDNA
CC   library. The fragments were amplified from the library using PCR primers
CC   based on the sequence of human genomic clones which hybridised with a
CC   murine delta receptor cDNA probe. Nucleotide probes derived from the
CC   kappa opioid receptor coding sequence are useful for diagnosis of
CC   neurological, cardio- vascular and psychiatric disorders associated with
CC   opioid receptors
XX
SQ   Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match   98.8%; Score 1140.4; DB 2; Length 1142;
Best Local Similarity   99.9%; Pred. No. 5.9e-270;
Matches 1141; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCCATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCGAGCGGCC   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCGAGCGGCC   60

Qy   61 TGCCTGCCCCCCAACAGCAGCGGCCCTGGTTTCCGGGCGTGGGCCGAGCCGACCAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCCAACAGCAGCGGCCCTGGTTTCCGGGCGTGGGCCGAGCCGACCAGCAACGGC 120

Qy   121 AGCGGCCGGCTCGGAGGACGCGGCCAGCAGCCGCCGGCACATCTCCCGGCCATCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCCGGCTCGGAGGACGCGGCCAGCAGCCGCCGGCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGGCCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGGCCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGACTTCCGACACACCCTTGAAGGCAAAGATCATCAATATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGACTTCCGACACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGAGGCACCAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||

Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTGTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCTGCAGTTCCCAGATGACTACTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCTGCAGTTCCCAGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGGCTTCGTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGGCTTCGTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTCGTCGTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCGTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCACAGCACAGCGTGCTCTTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCACAGCGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGCGTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCATTCTTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGCGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCTCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCTCGTTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TG 1142
              ||
Db   1141 TG 1142

Search completed: April   6, 2005, 13:53:15
Job time : 703.667 secs

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OM nucleic - nucleic search, using sw model

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:   April  6, 2005, 12:28:42 ; Search time 215 Seconds
                                      (without alignments)
                         8782.620 Million cell updates/sec

Title:          US-09-904-584-3
Perfect score:  1154
Sequence:       1 atggactcccgatccagat.........ccagtatgactagtcgtgga 1154
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents NA:*
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        4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
        5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
        6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1144.4	99.2	1182	4	US-09-016-434-1417	Sequence 1417, Ap
2	1141.4	98.9	1143	4	US-09-341-446B-1	Sequence 1, Appli
3	1140.4	98.8	1142	3	US-08-765-743-1	Sequence 1, Appli
4	1136.2	98.5	1284	4	US-09-341-446B-3	Sequence 3, Appli
5	1130.2	97.9	1143	4	US-09-826-509-542	Sequence 542, App
6	999.4	86.6	1275	4	US-09-341-446B-5	Sequence 5, Appli
7	994.6	86.2	1275	4	US-09-341-446B-7	Sequence 7, Appli
8	912.4	79.1	1408	4	US-09-214-904-5	Sequence 5, Appli
9	912.4	79.1	1410	3	US-08-147-592A-1	Sequence 1, Appli
10	912.4	79.1	1410	3	US-08-292-694A-1	Sequence 1, Appli
11	869.6	75.4	1000	3	US-08-147-592A-11	Sequence 11, Appl
12	869.6	75.4	1000	3	US-08-292-694A-11	Sequence 11, Appl
13	449.6	39.0	2135	4	US-08-430-286A-1	Sequence 1, Appli
14	448	38.8	1618	3	US-08-889-108-1	Sequence 1, Appli
15	448	38.8	1618	3	US-08-889-108-3	Sequence 3, Appli
16	448	38.8	1618	3	US-08-120-601B-1	Sequence 1, Appli
17	448	38.8	1618	3	US-08-120-601B-3	Sequence 3, Appli
18	448	38.8	1618	5	PCT-US94-10358-3	Sequence 3, Appli
19	448	38.8	1618	5	PCT-US94-10358-3	Sequence 3, Appli
20	436.4	37.8	1610	5	PCT-US94-10358-7	Sequence 7, Appli
21	436.4	37.8	1610	3	US-08-188-275A-1	Sequence 1, Appli
22	436.4	37.8	2160	3	US-09-351-198-1	Sequence 1, Appli
23	436.4	37.8	2162	3	US-09-113-426-1	Sequence 1, Appli
24	436.4	37.8	2162	4	US-09-016-434-1379	Sequence 1379, Ap
25	436.4	37.8	2162	4	US-09-355-709C-7	Sequence 7, Appli
26	436.4	37.6	2162	4	US-09-761-962A-3	Sequence 3, Appli
27	434	37.6	1334	4		
28	434	37.6	1365	4	US-09-761-962A-11	Sequence 11, Appl
29	434	37.6	1423	4	US-09-761-962A-1	Sequence 1, Appli
30	434	37.6	1610	4	US-09-761-962A-16	Sequence 16, Appl
31	434	37.6	1729	4	US-09-761-962A-9	Sequence 9, Appli
32	434	37.6	2045	4	US-09-761-962A-10	Sequence 10, Appl
33	433.2	37.5	1182	4	US-09-826-509-546	Sequence 546, App
34	433.2	37.5	1203	4	US-09-826-509-544	Sequence 544, App
35	432.4	37.5	2229	4	US-09-214-904-1	Sequence 1, Appli
36	430.8	37.3	1542	4	US-09-761-962A-4	Sequence 4, Appli
37	430.8	37.3	1981	3	US-08-387-707-15	Sequence 15, Appl
38	430.8	37.3	1981	3	US-08-405-271A-15	Sequence 15, Appl
39	424.2	36.8	1829	2	US-08-411-859-1	Sequence 1, Appli
40	424.2	36.8	1829	3	US-08-387-707-7	Sequence 7, Appli
41	424.2	36.8	1829	3	US-08-405-271A-7	Sequence 7, Appli
42	424.2	36.8	2218	4	US-09-214-904-3	Sequence 3, Appli
43	424.2	36.8	2219	4	US-08-432-174A-1	Sequence 1, Appli
44	424.2	36.8	2272	3	US-08-147-592A-3	Sequence 3, Appli
45	424.2	36.8	2272	3	US-08-292-694A-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-09-016-434-1417
; Sequence 1417, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;     APPLICANT: Janice Au-Young
;     APPLICANT: Jeffrey J. Seilhamer
;     TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;     TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;     NUMBER OF SEQUENCES: 1490
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;        STREET: 3174 PORTER DRIVE
;        CITY: PALO ALTO
;        STATE: CALIFORNIA
;        COUNTRY: USA
;        ZIP: 94304
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/016,434
;        FILING DATE: HEREWITH
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:
;        FILING DATE:
;        CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Zeller, Karen J.
;        REGISTRATION NUMBER: 37,071
;        REFERENCE/DOCKET NUMBER:  PA-0002 US
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (650) 855-0555
;        TELEFAX:  (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1417:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 1182 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;        LIBRARY: GENBANK
;        CLONE: g532059
US-09-016-434-1417

  Query Match             99.2%;  Score 1144.4;  DB 4;  Length 1182;
  Best Local Similarity   99.5%;  Pred. No. 7.4e-284;
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Matches 1148;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCCGCCCGAGCGCC  60
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Db    14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGCCCTACCTGCCGCCCGAGCGCC  73

Qy    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCGGC 120
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Db    74 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCGGC 133

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCCGCACATCTCCCGGCCATCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCCGCACATCTCCCGGCCATCCGGTC 193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCACTTG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCACTTG 373

Qy   361 ATGAATTCCTGGCCTTTGGGGATGCTGTGTCAAGATGTAATTTCCATTGATTACTAC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTGGGGATGCTGTGTCAAGATGTAATTTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGGACCGCGCTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGGACCGCGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTGTCGTCATCGTGGCATCTTCTGCAATAGTCCTTGAGGCACCAA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTGTCGTCATCGTGGCATCTTCTGCAATAGTCCTTGAGGCACCAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACCTTCGTCGTCGTGACTCCGTCTTCATCTTTGCTTCGTCGTCTTGTCCTC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCTTCGTCGTCGTGACTCCGTCTTCATCTTTGCTTCGTCGTCTTGTCCTC 733

Qy   721 ATCATCACGGGCGGTCTACTCCGTGATGATCCGCTCTCAAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCACGGGCGGTCTACTCCGTGATGATCCGCTCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy   781 ATGTTCGTGATCATCCGATACACAAAGATCACCAGACTCGTGTCTTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 ATGTTCGTGATCATCCGATACACAAAGATCACCAGACTCGTGTCTTGGTGGTG 853

Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCATCCTTGGTGGAGGCTCTGGGGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTCTGCTGGACTCCCATTCATCCTTGGTGGAGGCTCTGGGGG 913

Qy   901 AGCACCTCCACAGCAGCAGCGTGCTCTCTCCTCCAGCTATTCTCTGCCTTAGGCTAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCACAGCAGCAGCGTGCTCTCTCCTCCAGCTATTCTCTGCCTTAGGCTAT 973

Qy   961 AACAAGTTCACCAGCATCTTCACCTTGACCGTGACCGTGGACCGCGCTACATTGCCGTG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 AACAAGTTCACCAGCATCTTCACCTTGACCGTGACCGTGGACCGCGCTACATTGCCGTG 1033

Qy  1021 TTCCCGGGACTTCTGCTTTCTGCTTTCCACTGAAGATGAGGCGCAGAGTGAGGCGCAGAGTC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTCCCGGGACTTCTGCTTTCTGCTTTCCACTGAAGATGAGGCGCAGAGTGAGGCGCAGAGTC 1093

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAAACCAGTA 1153

Qy  1141 TGACTAGTCGTGGA 1154
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Db  1154 TGACTAGTCGTGGA 1167
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RESULT 2

US-09-341-446B-1

; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens

US-09-341-446B-1

Query Match   98.9%;   Score 1141.4;   DB 4;   Length 1143;
Best Local Similarity 99.9%;   Pred. No. 4.3e-283;
Matches 1142;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCCGCCCGAGCGCC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCCGCCCGAGCGCC  60

Qy    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCGGC 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCCGCACATCTCCCGGCCATCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGCGCAGCTGAGCCCGCCGCACATCTCCCGGCCATCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCACTTG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCACTTG 360

Qy   361 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCCTTGGTGGGCAACTTCGCTGGTC 420

Qy   421 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 480
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Db   421 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACCAACATTTACATATTTAAC 480

Qy   481 TGCCACCCCGTGAAGGCTTTCCGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db   481 TGCCACCCCGTGAAGGCTTTCCGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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APPLICATION NUMBER: FR 94/08531
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00912
FILING DATE: 07-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: NX 1758-1P US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1142 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1142
US-08-765-743-1

Query Match   98.8%;   Score 1140.4; DB 3;   Length 1142;
Best Local Similarity 99.9%;   Pred. No. 7.8e-283;
Matches 1141; Mismatches 0; Conservative 0; Indels 1; Gaps 0;

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Qy     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCTTCCGCGGCCCCGAGCGCC    60
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Db     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGCCGGGCCCTTCCGCGGCCCCGAGCGCC    60

Qy    61 TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTTCCCGGCGCCTGGCGCCCGACAGCAACGGC   120
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Db    61 TGCCTGCCCCCAACAGCAGCGCCGCCTGGTTTCCCGGCGCCTGGCGCCCGACAGCAACGGC   120

Qy   121 AGGGCCGGCTCGGAGGACGCGCAGCTGAGCCGCGCACATCTCCCGCGCCATCCGGTC     180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGGGCCGGCTCGGAGGACGCGCAGCTGAGCCGCGCACATCTCCCGCGCCATCCGGTC     180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGCAACTCGCTGGTC    240
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Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGCAACTCGCTGGTC    240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC   300

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360
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Db   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   420
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Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACGGTGACATTGCCGTG   480
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Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACGGTGACATTGCCGTG   480

Qy   481 TGGCACCCCGTGAAGGCTTTGGACTTCCGCCACACCCTTGAAGGCAAAGATCATCAATATC   540
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Db   481 TGGCACCCCGTGAAGGCTTTGGACTTCCGCCACACCCTTGAAGGCAAAGATCATCAATATC   540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGCATCCTCTGCAATAGTCCTTGGAGGCACCAAA   600
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Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGCATCCTCTGCAATAGTCCTTGGAGGCACCAAA   600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCCCAGATGATGACTACTCC   660
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Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCCCAGATGATGACTACTCC   660

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGGAGGCACCAAA   600
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Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGGAGGCACCAAA   600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCCCAGATGATGACTACTCC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTCTCCCCAGATGATGACTACTCC   660

Qy   661 TGGTGGGACCCTCTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTC   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCCTCTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTC   720

Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780
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Db   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG   840
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Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG   840

Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGGAGGCTCTGGGG   900
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Db   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGGAGGCTCTGGGG   900

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTGCTCTTCTCCAGTTACTTCTCTGATGAAAACTTCAAGCCGTGT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTGCTCTTCTCCAGTTACTTCTCTGATGAAAACTTCAAGCCGTGT  1020

Qy   901 AGCACCTCCCACAGCACAGCTGTCTCTCTAGGCTTTAT     960
           ||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGCTGTCTCTCTAGGCTTTAT     960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCCGTGT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCCGTGT  1020

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCAGAGCCACTAGCAGAGTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGCAGAGCCACTAGCAGAGTC  1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy  1141 TGA   1143
           ||
Db  1141 TGA   1143
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RESULT 3
US-08-765-743-1
; Sequence 1, Application US/08765743
; Patent No. 6146835
GENERAL INFORMATION:
APPLICANT: KIEFFER, Brigitte
APPLICANT: SIMONIN, Frederic
TITLE OF INVENTION: HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC
TITLE OF INVENTION: ACIDS AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,743
FILING DATE: 11-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

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Qy   661  TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGTGATCCCTGTCCTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCGTGATCCCTGTCCTC  720

Qy   721  ATCATCATCTGCTGCTACACCCTGCGTCTCGTCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATCATCATCTGCTGCTACACCCTGCGTCTCGTCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGTGGTG  840

Qy   841  GCAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGG  900

Qy   901  AGCACCTCCCACAGCAGCAGTCGCTCTCTCCTACGCCTTTCTTGATGAAAACTTCAAGCGTGTT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AGCACCTCCCACAGCAGCAGTCGCTCTCTCCTACGCCTTTCTTGATGAAAACTTCAAGCGTGT  960

Qy   961  ACCAACAGTAGCCTGAATCCCATTCCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  ACCAACAGTAGCCTGAATCCCATTCCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT  1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTCC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTCC  1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGGACATCGATGGGATGAATAAACCAGTA  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141 TG  1142
          ||
Db   1141 TG  1142
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RESULT 4
US-09-341-446B-3
; Sequence 3, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
US-09-341-446B-3

Query Match 98.5%; Score 1136.2; DB 4; Length 1284;
Best Local Similarity 99.7%; Pred. No. 9.8e-282;
Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy   2    TGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCTCACCTGCGCCCCGAGCGCCT  61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113  TCGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCTCACCTGCGCCCCGAGCGCCT  172

Qy   62   GCCTGCCCCCAAACAGCAGCGCCCTGGTTTCCCGGCGCTGGGCCCGAGCAGCAACGGCA  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233  GCGCCGGCTCGGAGGACGCGCCAGCTGGAGCGGCCGCCGCCGCCACATCTCCCGGCATCCCCGGTCA  292
```

```
Db   173  GCCTGCCCCCAAACAGCAGCGCCCTGGTTTCCCGGCGCTGGGCCCGAGCAGCAACGGCA  232

Qy   122  GCGCCGGCTCGGAGGACGCGCCAGCTGGAGCGGCCGCCGCCGCCACATCTCCCGGCATCCCCGGTCA  181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233  GCGCCGGCTCGGAGGACGCGCCAGCTGGAGCGGCCGCCGCCGCCACATCTCCCGGCATCCCCGGTCA  292

Qy   182  TCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGGCTGGCAACTCGCTCGTCA  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293  TCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGGCTGGCAACTCGCTCGTCA  352

Qy   242  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACC  412

Qy   302  TGGCTTGGCAGATGCTTTAGTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA  361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413  TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA  472

Qy   362  TGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTACA  421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473  TGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTACA  532

Qy   422  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTGT  481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   533  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTGT  592

Qy   482  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGGCAAAGATCATCAATATCT  541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   593  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGGCAAAGATCATCAATATCT  652

Qy   542  GCATCTGGCTGCTGTCGTCGTCATCCTGGCATCCTCTGTCAATAGTCCTTGGAGGCACCAAAG  601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653  GCATCTGGCTGCTGTCGTCGTCATCCTGGCATCCTCTGTCAATAGTCCTTGGAGGCACCAAAG  712

Qy   602  TCAGGGAAGACGTCATGTCATTGAGTGCTTCCTTGCAGTTCCCAGTTCCCAGTCCTCCTGATGACTACTCCT  661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   713  TCAGGGAAGACGTCATGTCATTGAGTGCTTCCTTGCAGTTCCCAGTTCCCAGTCCTCCTGATGACTACTCCT  772

Qy   662  GGTGGGACCTTCTTCATGAAGATCTGCGTCTCGTCTTGCCTTCGTGATCCCGGCTCCTTTCTG  721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   773  GGTGGGACCTTCTTCATGAAGATCTGCGTCTCGTCTTGCCTTCGTGATCCCGGCTCCTCA  832

Qy   722  TCATCATCGTCTGCTACACCCTGATCATCCGGCTCTGATGATCCTGCGCTCGTCTCAAGAGCGTCCGGCTCCTTTCTG  781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   833  TCATCATCGTCTGCTACACCCTGATCATCCGGCTCTGATGATCCTGCGCTCGTCTCAAGAGCGTCCGGCTCCTTTCTG  892

Qy   782  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGTGGTGG  841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   893  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGTGGTGG  952

Qy   842  CAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGA  901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   953  CAGTCTTCGTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGA  1012

Qy   902  GCACCTCCCACAGCACAGCAGTCGCTCTCTCTCCAGCTATTACTTCTGATCATCGATCATCCGCCTTCTCACGCCGCCTTAGGCGTATA  961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 GCACCTCCCACAGCACAGCAGTCGCTCTCTCTCCAGCTATTACTTCTGATCATCGATCATCCGCCTTCTCACGCCGCCTTAGGCGTATA  1072

Qy   962  CCAACAGTAGCCTGAATCCCATTCCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 CCAACAGTAGCCTGAATCCCATTCCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1132

Qy   1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTCC  1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTCC  1192

Qy   1082 GAAATACAGTTCAGGATCCTGCTTACCTGGACATCGATGGGATGAATAAACCAGTAT  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 GAAATACAGTTCAGGATCCTGCTTACCTGGACATCGATGGGATGAATAAACCAGTAG  1252

Qy   1142 G  1142
          |
Db   1253 G  1253
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Db    601  GTCAGGGAAGAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy    661  TGGTGGGACCTCTTGCTGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TGGTGGGACCTCTTGCTGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720

Qy    721  ATCATCATCGTCGTCTACACCCTGATGATCCTGCTCTCGAAGAGCGTCCGGCTCTCCTTCT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATCATCATCGTCGTCTACACCCTGATGATCCTGCTCTCGAAGAGCGTCCGGCTCTCTTTCT  780

Qy    781  GGCTCCCCAGAGAAGAGATCGCAACCTGCGTAGGAATCACCAGACTGGTCTCGGTGGGTG  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTCCCCAGAGAAGAGATCGCAACCTGCGTAGGAATCAAGAGACTGGTCCTGGTGTGGGTG  840

Qy    841  GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGAGGCTCTGGGG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG  900

Qy    901  AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960

Qy    961  ACCAACAGTAGCCTGAATCCCATTCTTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  ACCAACAGTAGCCTGAATCCCATTCTTCACGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy   1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141  TGA  1143
           |||
Db   1141  TGA  1143
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RESULT 6
US-09-341-446B-5
; Sequence 5, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of a G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASSL OR1
US-09-341-446B-5

Query Match   86.6%; Score 999.4; DB 4; Length 1275;
Best Local Similarity 93.0%; Pred. No. 1.3e-246;
Matches 1061; Conservative   0; Mismatches 71; Indels   9; Gaps   1;

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Qy     2  TGGACTCCCGATCCAGATCTTCGGGGGAGCCGGGCCCCACCTGCCCCGCCCCGAGCGCCT   61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113  TCGACTCCCCGATCCGATCTTCCGGGGAGCCGGGCCCCGGGCCCCACCTGCCCCGCCCCGAGCGCCT  172
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RESULT 5
US-09-826-509-542
; Sequence 542, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 542
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-542

Query Match   97.9%; Score 1130.2; DB 4; Length 1143;
Best Local Similarity 99.3%; Pred. No. 3.2e-280;
Matches 1135; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Qy     1  ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCCCGGCCCTACCTGCCCCGAGCGCC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGGAATCCCGATTCAGATCTTCAGATCTTCCGCGGGAGGAGCCCGGCCCTACCTGCCCCGAGCGCC   60

Qy    61  TGCCTCGCCCCAACAGCAGCGCCTGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TGCCTCGCCCCAACAGCAGCGCCTGTTCCCGGCTGGGCCGAGCCCGACAGCAACGCGGC  120

Qy   121  AGCGCCGGCTCGGAGACGCGGCAGCGCGGACGGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AGCGCCCGGCTCGGAGACGCGGCAGCGCGGACGGCTGGAGCCCGCACATCTCCCCGGCCATCCCGGTC  180

Qy   181  ATCATCACGGACGGTCTACTCCCGTAGTGTTCGTCGTGGGCTGGTGGGCCAACTCGCTGGTC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATCATCACGGCGGTGGTCTACTCCCGTAGTGTTCGTCGTGGGCTGGTGGGCCAACTCGCTGGTC  240

Qy   241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy   301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGACCGGTCTACTTG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGACCGGTCTACTTG  360

Qy   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATGAGCCGGTGGCAATTGTTCCATGATTACTAC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATGAGCCGGTGGCAATTGTTCCATGATTACTAC  420

Qy   421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGCTACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGCTACATTGCCGTG  480

Qy   481  TGCCACCCCGTGAAGGCTTTGGACTTCGGCAAACACCCGACACACCCTTGAAGGCAAGATCATCAATATC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TGCCACCCCGTGAAGGCTTTGGACTTCGGCAAACACCCGACACACCCTTGAAGGCAAGATCATCAATATC  540

Qy   541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTCTCCAATAGTCCTTGGAGGCACCAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTTGGCATCTCTCCAATAGTCCTTGGAGGCACCAAA  600

Qy   601  GTCAGGGAAGAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Db   1244 G 1244

RESULT 7
US-09-341-446B-7
; Sequence 7, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RASSL OR2
US-09-341-446B-7

Query Match   86.2%; Score 994.6; DB 4; Length 1275;
Best Local Similarity   92.7%; Pred. No. 2.2e-245;
Matches 1058; Conservative 0; Mismatches 74; Indels 9; Gaps 1;

[DNA sequence alignment follows, with Qy (query) and Db (database) rows numbered from 2/113 through 1142/1244]

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;          LOCATION:  184..1323
US-09-214-904-5

Query Match        79.1%;  Score 912.4;  DB 4;  Length 1408;
Best Local Similarity  86.9%;  Pred. No. 3e-224;
Matches 1003;  Conservative  0;  Mismatches 151;  Indels  0;  Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGAGGAGCCGGGCCTACCTGCCCCCGAGCGCC  60
            |||||||||||||||||  || ||||||  ||||||||||||||||||||||||||||
Db    184 ATGGAGTCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCCAGTGCT 243

Qy     61 TGGCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCTGGCCGAGCCCGACAGCAACGGC 120
            ||||| | |||||||||||||||| ||||||  |||||  |||||||  |||||||
Db    244 TGCCTTCTCCCAACAGCAGCAGCTCTTGGTTCCCAACTGGCAGAATCCGACAGTAATGGC 303

Qy    121 AGGGCCGGCTCGGAGGACCAGCGCAGCTGGAGCGGCACATCTCCCGGCCATCCCGGTC 180
            |||  |  | ||| |||| ||||| |||||||||||  ||||| ||||||  || ||
Db    304 AGTGTGGGGCTCAGAGGATCAGCAGCTCGAGTCGGCCCATCCTCCGGCCATCCCTGTT 363

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGCGAACTCGCTGGTC 240
            ||||||| | || | |||||  |||||||||||||||||  ||||| ||  || ||||
Db    364 ATCATCACCGCGTCTGTCTACTCCGTGTGGTATTGTGCGGGGCTTAGTGGGGCAATTCTCGGTC 423

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
            |||||| ||| || ||  || ||| ||||||| ||  |||||||| ||||| |||||||
Db    424 ATGTTTGTCATCATCCGATACACGAAGATGAAGACCCGCAACCAACATCTACATATTTAAC 483

Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG 360
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    484 CTGGCTTTGGCAGATGCTTGGTTACTACAACCATGCCCTTCAGAGTGCGTCTACTTG 543

Qy    361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 420
            |||||||||||||||||| |||||||||||| |||||||  |||||||  ||||||||||
Db    544 ATGAATTCTTGGCCTTTTGGGAGATGTGCTGTATGCAAGATTGTCATTTCCATTGACTACTAC 603

Qy    421 AACATGTTCACCAGCACATTCACCCTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 480
            ||||||||| |||||| ||||| ||||||||||||| ||||||||||||| || || |||
Db    604 AACATGTTTACCAGCATATTCACCTTTGACCTTCCGAACACCCTTGAAAGCAAAGATCATCAACATC 663

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCCATCCTCTGGCATCCTCTGTTGGAGGCACCAAA 540
            ||||||||||||||||||||| |||||| |||  |||||||||||||||||||||||||||
Db    664 TGCCACCCCGTGAAAGCTTTGGACTTCCTGTATATCAGGGATAGTCCTTGGAGGCACCAAA 723

Qy    541 TGCATCTGGCTGCTGCTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGACTACTCC 600
            ||||| |||||||||||| |||||||||||||| ||| ||||||||||||||||||||||
Db    724 TGCATTTGGCTGCCTGGCATCATCGTTGGTATATCAGGGATAGTCCTTGGAGGACCAAA 783

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTCGTCCTGAGTTCCAGATGATGACTACTCC 660
            || | |||||||||||||||||| | | |||||||||| |||||||||||||||||
Db    784 GTCAGGGAAGATGTGGATGTCATTGAATGCTCCTGAGTTCCTGATGATGAATATTCC 843

Qy    661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTCGTCGTCCCTGTCCTC 720
            |||||||||||| ||||||||||||  |||| | | |||||||| ||||||||
Db    844 TGGTGGGATCTCTTCATGAAGATCGTGTCTTCGTCTTTGTCGTCCCTTGTGATCCCCAGTCCTC 903

Qy    721 ATCATCATCGTCGTCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
            |||||||||| | || ||||||||||||||||||  |||||||||||||||||||||| |
Db    904 ATCATCATTGTCGTCTACACCCCCGATGATCCTGCGCCCGAAGAGTGTCCGGCTCCTGTCT 963

Qy    781 GGCTCCCGAGAAAAGATCGCAACCTGCCTAGGATCACCAGGCTCCTGGTGGTGGTG 840
            |||||||||||||| |||  |||||||| | ||||||||||||||||||||||||||
Db    964 GGCTCCCGAGAGAAGACCGGAATCTCCGCCGCCATCACCAAGCTGGTCGGTAGTAGTT 1023

Qy    841 GCAGTCTTCGTCTGTGGACTCCATTCACATATTCATCTTGGTGGAGGCTCTGGGG 900
            | ||||||| |||||||||| ||||||||||  ||||  ||||||||||||| |
Db   1024 GCAGTCTTCATCATCGTGTGACCCCCATTCACATCATCTTTATCCTGGTGGAGGCTCTGGGA 1083

Qy    901 AGCACCTCCCACAGCACCAGCTGCTCCTCCCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
            ||||| |||| ||||| | ||  ||||| ||| |||| |||||||| |||| ||| ||||
Db   1084 AGCACCTCCCACAGCACAGCTGCCCTCCTCCAGCTATTATTTCTGCATTATTATTGCCTTGGGGTTAT 1143

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTGATGAAAACTTCAGCGGTGT 1020
            |||  ||||||||||  |||  || | |  ||  || ||| |||||||||| |||||||||
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Qy    602 TCAGGGAAGACGTCGATGTCATTGAGTCGTCCTTGCAGTTCCCAGATGATGACTACTCCT 661
            || |||||  || | || | |||| ||| ||| ||                  ||| ||
Db    713 CCCGGGATGGAGCAGTGGTATGCAGAGATCGGCTTCCCAGTTCCCAGCCC-------CAGCTGGT 763

Qy    662 GGTGGGACCTCTTCATGAAGAATCGCGGTCTTCGTCTTCGTCGTCCCTGTCCTCA 721
            |||| || |||||||| ||| | ||| |||||| | |||||| ||| |||| || 
Db    764 ACTGGGACACTGTGACCAAGATCGCGGTCTTCGTCATCGTTCCGTCGTCCCTGTCCTCA 823

Qy    722 TCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGGTCCTGGTGGTGGTGG 781
            |||||||||  | |||||||| ||||||||||  ||||| |||||||||||||| |||||
Db    824 TCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGACTGGTCCTTTCTG 883

Qy    782 GCTCCCGAGAGAAAGATCGCAACCTGCCGTAGGATCACCAGGATCCTGGTCCTGGTGGTGG 841
            |||||||||||||||||||||||||| || ||||||||||||| |||||| |||| ||||
Db    884 GCTCCCGAGAGAAAGATCGCAACCTGCCGTAGGATCACCAGGAGACTGGTCCTTGGTGGTGG 943

Qy    842 CAGTCTTCGTCGTCTGGACTCCCCATTCCATTCACATATTCACATATTCACTCGTGGAGGCTCTGGGGA 901
            ||||||||||||||||||||  | || | |||||||||||| || ||| || | |||||||||
Db    944 CAGTCTTCGTCGTCTGGACTCCCCATTCCATTCACATATTCACATCTGCGTGGAGGCTCTGGGGA 1003

Qy    902 GCACCTCCCACAGCACACAGCTGCTCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTATA 961
            ||||||||||||| |||||| ||||| | |||||||||||||||||||||| ||||||||||
Db   1004 GCACCTCCCACAGCACACAGCTGCTGATCTTCCAGCTATTACTTCTGCATTGCCTTAGGCTATA 1063

Qy    962 CCAACAGTAGCCTGAATCCCATTCCATTCCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT 1021
            |||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db   1064 CCAACAGTAGCCTGAATCCCATTCCATTCCTTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT 1123

Qy   1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTCC 1081
            |||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db   1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTCC 1183

Qy   1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAT 1141
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1184 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAG 1243

Qy   1142 G 1142

Db   1244 G 1244
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RESULT 8
US-09-214-904-5
; Sequence 5, Application US/09214904
; Patent No. 6632977
;         GENERAL INFORMATION:
;          APPLICANT:
;          TITLE OF INVENTION:   TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
;          TITLE OF INVENTION:   OF OPIATE RECEPTORS IS MODIFIED
;          NUMBER OF SEQUENCES:  6
;          COMPUTER READABLE FORM:
;           MEDIUM TYPE:  Floppy disk
;           COMPUTER:  IBM PC compatible
;           OPERATING SYSTEM:  PC-DOS/MS-DOS
;           SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;          CURRENT APPLICATION DATA:
;           APPLICATION NUMBER:  US/09/214,904
;           FILING DATE:
;          PRIOR APPLICATION DATA:
;           APPLICATION NUMBER:  PCT/FR97/01282
;           FILING DATE:
;           APPLICATION NUMBER:  FR 96.08810
;           FILING DATE:  15-JUL-1996
;          INFORMATION FOR SEQ ID NO: 5:
;          SEQUENCE CHARACTERISTICS:
;           LENGTH:  1408 base pairs
;           TYPE:  nucleic acid
;           STRANDEDNESS:  double
;           TOPOLOGY:  linear
;          MOLECULE TYPE:  DNA (genomic)
;          FEATURE:
;           NAME/KEY:  CDS
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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCGGGGCCCTACCTGCGCCCCGAGCGCC   60
         ||||| ||||| || |||||||||||||       ||||||||||||| || ||| |||
Db   186 ATGGAGTCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTACCTGCTGCTCCCAGTGCT   245

Qy    61 TGCCTGCCCCGCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCAGCCCCGACCAGAGGC  120
         ||||| |||| ||||||||||||||| |||||| |||  ||||||||||| ||| ||
Db   246 TGCCTTCTCCCAACAGCAGCAGCTCTTGGTTCCCAACTGGGCCAGCAGCAGTAATGGC   305

Qy   121 AGCGCCGGTCGGAGGACGCGCAGCTGGACCAGCAGCGAGTCCGCGCCACATCTCCCGGTC  180
         || |||||| |||||||  |||||||||||||| |||||||||  ||||||||| |||||
Db   306 AGTGTGGGGCTCAGAGATCAGCAGCTGGACCAGCAGCGAGTCCGGCCATCCCGTT   365

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCCTTGTGGGCAACTGCTGGTC  240
         |||||| ||| |||| ||| || |||||  ||||||| || |||||| |||||||||||
Db   366 ATCATCACCGTGTCTACTCCGTAGTGTTTGTGGGCCTTAGTGGGCAATTCTCTGGTC   425

Qy   241 ATGTTCGTGATCATCCGATCACAAAGATGAAGACAGCACCAACATTTACATATTTAAC  300
         |||||| ||| ||||| |||||||||||| ||||||||| |||||  ||||| ||||||
Db   426 ATGTTTGTCATCATCCGATCACGAGAGATGAAGACCGCAACCAACATCTACATATTTAAC   485

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360
         ||||||||||| ||||| |||||| ||||| ||||| |||||||||| ||| |||||||
Db   486 CTGGCTTTGGCAGATGCTTTTGGTTACTACCACTATGCCCTTCAGAGTGCTGTCTACTTG   545

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCATTGATTACTAC  420
         |||||||| |||| |||| |||||||| ||||||||| ||||| |||||| || |||||
Db   546 ATGAATTCTTGGCCTTTTGGGGATGCTGTCATGCAAGAGTTGTCATTTCCATTGACTACTAC   605

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG  480
         |||||||| ||||| || ||||| ||||||||||||| || |||| |||| |||||| |
Db   606 AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGACCGCTACATTGCTGTG   665

Qy   481 TGCCACCCCTGAAGGCTTTGGACTTCCGCACACCCTTGAAAGGCAAAGATCATCAATATC  540
         |||| |||| ||||||||| |||| ||| |||| |||||||| |||||||| |||| |
Db   666 TGCCACCCTGAAGGCTTTTGGACTTCCGCAACACCTTTGAAAGCAAAGATCATCAACATC   725

Qy   541 TGCATCTGGCTGCTCGTGTTGGCATCTGTCAAGATAGTCATTGATGATGACTACTAC  600
         |||| ||||| || |||| || |||| || ||||| || ||||||| || |||||
Db   726 TGCATTGGCTGCTCGTGTTGGCATCATCGTGTATATCAGCGATAGTCATTGTCATTGATTACTAC   785

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC  660
         ||||||| ||| |||| ||||  || ||||| || ||||| || ||||| |||||||
Db   786 GTCAGGGAAGATGTGGATGTCATTGAAATGCTCCTTGCAGTTTCCTGATGATGAATATTCC   845

Qy   661 TGGTGGACCCTTCATGAAGATCGCGGTCTTCATCTTTGCCTTCGTGCCCTGTCGTCCCTC  720
         |||| |||||| ||||| ||| ||| || ||||| ||||| |||| | |||||||||
Db   846 TGGTGGGATCTCTTCATGAAGATCTGTGTCTTTGCCTTTGTGCCTTTGTGATCCCAGTCCTC   905

Qy   721 ATCATCATCGTTCTGCTACACCCTGATGATCCTGCCGTCTCAAGAGCGTCCGGCTCCTTCT  780
         ||||||||| ||||||| |||||||||||||||| |||||||||||| ||||| ||||||
Db   906 ATCATCATTGTTCTGCTACACCCTGATGATCCTGCCGTCTCAAGAGAGTGTCCGGCTCCTGTCT   965

Qy   781 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACCTGGTCCTGGTGGTG  840
         ||||||||||||||||| || ||||| |||||| |||| ||||| ||||||||||||
Db   966 GGCTCCCGAGAGAAGAGACCGAAATCTCCGCGCAATCCAACAGCTGGTCGTGCTGTAGTAGTT  1025

Qy   841 GCAGTCTCGTCGTCCTGGACTCCCATTCATCCTGTGGAGGCTCTGGGG  900
         ||||| ||||| |||||||||||||||| |||| |||||||||||| |
Db  1026 GCAGTCTTCATCATCGTTGTTGGACCCCCATTCTCCAGCATTGCCTTAGGCTAT   1085

Qy   901 AGCACCCTCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTCGATGGCTCTTAGGCTAT  960
         ||||| |||| ||||| |||||| |||||| ||||||| ||| |||| |||||||||||
Db  1086 AGCACCTCCACCAGCAGCAGCGCCCCTCTCCCAGCTATTATTTCTCGTTATTGCCTTGGGTTAT  1145

Qy   961 ACCAACAGTAGCTGCAATCCCATTCTTCTAGGCCTTTCTTGATGAAAAACTTCAAGCCGGTGT 1020
         ||||| ||||||| |||| |||||| ||| ||||||||||| || |||| ||||||| |||
Db  1146 ACCAACAGCAGCGCCTGAATCCTGTTCTTCTATGCCTTTCTGATGATGAAAACTTCAAGCGGTGT 1205

Qy  1021 TTCCGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGGCGGCAGAGCACTAGCAGAGTC 1080
         || | |||||| |||| ||||| ||| |||| || ||||| || ||||| || ||||||
Db  1206 TTTAGGGACTTCTCGTTTCCCTATTAAGATGGAATTGGAGTCGGCCAGAGCACCAATAGAGTT 1265

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
         | |||| ||||| || ||||| |||| ||||| |||| ||||| || ||||| |||||||
Db  1144 ACCACAGCAGCCTGAATCCTGTTCTGATGAAAACTTCAAGCGGTGT 1203

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGGCGGCAGAGCACTAGCAGAGTC 1080

Db  1204 TTTAGGGACTTCTCGTTTCCCTATTAAGATGGAATTGGAGTCGGCCAGAGCACCAATAGAGTT 1263

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Db  1264 AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGGAGGGATGAATAAGCCAGTA 1323

Qy  1141 TGACTAGTCGTGGA 1154

Db  1324 TGACTAGTCGTGGA 1337
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RESULT 9

US-08-147-592A-1

; Sequence 1, Application US/08147592A
; Patent No. 6096513

GENERAL INFORMATION:
  APPLICANT: Bell, Graeme I
  APPLICANT: Reisine, Terry
  APPLICANT: Yasuda, Kazuki
  TITLE OF INVENTION: Opioid Receptor Genes,
  TITLE OF INVENTION: Compositions and Methods
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: Texas
    COUNTRY: United States of America
    ZIP: 72210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/147,592A
    FILING DATE: 05-NOV-1993
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/100,694
    FILING DATE: 30-JUL-1993
    CLASSIFICATION: 435
    APPLICATION NUMBER: 08/066,296
    FILING DATE: 20-MAY-1993
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Wilson, Mark B.
    REGISTRATION NUMBER: 37,259
    REFERENCE/DOCKET NUMBER: ARCD:105
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (512) 418-3000
    TELEFAX: (512) 474-7577
    TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1410 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 186..1325

US-08-147-592A-1

Query Match 79.1%; Score 912.4; DB 3; Length 1410;
Best Local Similarity 86.9%; Pred. No. 3e-224;
Matches 1003; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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Db  1266 AGAAACACAGTTCAGGATCCTGCTTCAGGATCCTCCATGAGAGAATGTGGGAGGGATGAATAAGCCAGTA 1325
Qy  1141 TGACTAGTCGTGGA 1154
Db  1326 TGACTAGTCGTGGA 1339
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RESULT 10
US-08-292-694A-1
; Sequence 1, Application US/0829294A
; Patent No. 6319686
; GENERAL INFORMATION:
; APPLICANT: BELL, GRAEME
; APPLICANT: REISINE, TERRY
; APPLICANT: YASUDA, KAZUKI
; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,694A
; FILING DATE: August 19, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20 May 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30 July, 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/147,592
; FILING DATE: 5 No. 6319686ember 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US94/05747
; FILING DATE: 20 May 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MARK B. WILSON
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:140/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 186..1325
US-08-292-694A-1

Query Match   79.1%; Score 912.4; DB 3; Length 1410;
Best Local Similarity   86.9%; Pred. No. 3e-224;
Matches 1003; Mismatches 151; Conservative 0; Indels 0; Gaps 0;

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Qy     1 ATGGACTCCCCATCCAGATCTTCCGCGGGAGGAGCCGCGGGCCCTACCTGCGCCCCGAGCGCC 60
           |||||  |||||| |||||||||| ||  ||  || || || ||||||| ||||||  |||
Db   186 ATGGAGTCCCCATTCAGATCTTCCGAGGAGATCCAGGCGCCCTACCTGCTCCCCAGTGCT 245

Qy    61 TGGCTGCCCCACCAGCGGCTGGTTCCCGCGCTGGTCGCCGAGCCCGAGCAGCAACGGC 120
          ||||| ||||| |||| |||||||||| |  |||| |||||||||||| |||||| || 
Db   246 TGCCTTCTCCCCACAGCAGCTCTTGGTTCCCCAACTGGGCAGAATCCGACAGTAATGGC 305

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180
          |||| ||||||||||||| || ||||||||| || ||||||| |||||||||||||| 
Db   306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCGCGCCGCACATCTCCGGCCATCCCTGTT 365

Qy   181 ATCATCACGGCGCTACTCCGTAGTGTTCGTCGTGGCTTGGTCGGCAACTCGCTGGTC 240
          ||||||||  ||| ||||| |||||| ||||| |||  | |||||||| | ||||||| 
Db   366 ATCATCACCGCTGTCTACTCTGTGTATTTGTGCGGTGGGCTTAGTGGGCAATTCTCTGGTC 425

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
          ||||| ||||||||||||||||| ||||||||||| || ||||||||| ||||||| || 
Db   426 ATGTTTGTCATCATCCGATACACAGAAGATGAAGACCGACAACCAACATCTACATATTTAAC 485

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||| | |||||| ||| ||||||||||||||| | |||||||||| 
Db   486 CTGGCTTTGGCAGATGCTGGTTACTACCACTATGCCCTTTCAGAGTGCTGTCTACTTG 545

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTTGTGCAAGATAGTAATTCCATTGATTACTAC 420
          ||||||||  ||||||||||  ||||||| ||||||||| || ||||||||||| ||||| 
Db   546 ATGAATTCTTGGCCTTTTGGAGATGTGCTATGCAAGATTGTCATTTCCATTGACTACTAC 605

Qy   421 AACATGTTCACCGACATCTTCACCTTGACCATGATGAGCGGTGACCGGCTACATTGCCGTG 480
          ||||||||| ||| | || ||||||||||||||||||| | |||||||||||||||| ||| 
Db   606 AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGGCTACATTGCTGTG 665

Qy   481 TGCCACCCCGTGAAGGCTTTGAGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||| |||||||||||||| ||  | || || | ||||| |||||||||||| |||| 
Db   666 TGCCACCCTGTGAAGGCTTTGAGAACACTTTGAAAGCAAAGATCATCAACATC 725

Qy   541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCCTCTGGAACAAGTCCTGGAGGCACCAAA 600
          ||||| |||||  || || |||||||||| | |   | | ||| ||| |||||||||||| 
Db   726 TGCATTTGGCTCCTGGCATCATCGTTGGTATATCAGCGATAGTCCTTGGAGGCACCAAA 785

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCCCTGCAGTTCCCAGATGACTACTCC 660
          |||||||||||  ||||||||||||| ||||| |||||||||||| ||||| ||| |||| 
Db   786 GTCAGGGAAGATGGGATGTCATTGAATGCTCCCTGCAGTTCCTGATGATGAATATTCC 845

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTTCTTCATCTTGCCTTCGTGATCCTGTCCTC 720
          |||||||| |||||||||||||||||| || || || || |||| |||||||| |||| 
Db   846 TGGTGGGATCTCTTCATGAAGATCTGTGTCTTCGTCTTTGCCTTTGTGATCCTCCTC 905

Qy   721 ATCATCATCGTCTGCTACACACCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          |||||||| ||||||||||||||  |||||||||||  |||||| |||||||||||| ||| 
Db   906 ATCATCATTGTCTGCTACACACCCTGATGATCCTGCGGCTCCTGAAGAGTGTCCGGCTCCTGTCT 965

Qy   781 GGCTCCGGAGAGAAAGATCGCAACCTGCGTAGGATCCACACCGACTGGTCCTGGTCCTGGTGTG 840
          ||||||  ||||||| || |||| || ||| | ||| |||| | |||||| ||| ||| ||| 
Db   966 GGCTCCCGAGAGAAGGACGCAAATCTCCGCCGCATCACCAGGCTGGTGCTGGTAGTAGTT 1025

Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
          ||||||||| || || ||||||| ||||||||||| || ||||||||||||||||||||  
Db  1026 GCAGTCTTCATCATCTGTTGGACCCCCATTCACATTTATCATCCTGGTGGAGGCTCTGGGA 1085

Qy   901 AGACCTTCCACAGCACAGCTGCTTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
          ||  |||||||||||||||||| |||| ||||||||| |||||| || ||||| || ||| 
Db  1086 AGCACCTTCCACAGCACAGCTGCCTCTCCAGCTATTATTTCTGCTATTTTGCCTTGGGTTAT 1145

Qy   961 ACCAACAGTAGCCGAATCCCATTCTGCTTCTCACTGATGAAAACTTCAGGCGTGT 1020
          ||||||||  |||| ||||| || ||||| |  |||||||||||||||||||| || 
Db  1146 ACCAACAGCAGCCTCGAATCCTGTTCTCTATGCCTTTCTGTGATGAAAAACTTCAGGCGGTGT 1205

Qy  1021 TTCCGGGACTTCGTCTTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTC 1080
          || | ||||||| |||| |  |||| ||||| ||||| |||| |||||||| |||||| 
Db  1206 TTTAGGGACTTCTGCTTCCCTATTAAGATGGCAATGGACGGACCAGAGCACCAATAGAGTT 1265

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTCACCTGAGAGACATCGATGGGACATCGATGAATAAACCAGTA 1140
          ||||| |||||||||||||||||||||| ||||||| || || |  |||| |||||||||||| ||||||| 
Db  1266 AGAAACACAGTTCAGGATCCTGCTTCAGGATCCTCCATGAGAGAATGTGGGAGGGATGAATAAGCCAGTA 1325
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Qy      1141 TGACTAGTCGTGGA 1154
             |||||||||||||
Db      1326 TGACTAGTCGTGGA 1339


RESULT 11
US-08-147-592A-11
; Sequence 11, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
;  APPLICANT: Bell, Graeme I
;  APPLICANT: Reisine, Terry
;  APPLICANT: Yasuda, Kazuki
;  TITLE OF INVENTION: Opioid Receptor Genes,
;  TITLE OF INVENTION: Compositions and Methods
;  NUMBER OF SEQUENCES: 43
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 72210
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/147,592A
;   FILING DATE: 05-NOV-1993
;   CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30-JUL-1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20-MAY-1993
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:105
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: DNA
;  FEATURE:
;   NAME/KEY: N
;   LOCATION: 607-608, 642-643, 896, 906
;   IDENTIFICATION METHOD: N = A, C, G or T
;  FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 102..986
;  FEATURE:
;   NAME/KEY: Xaa
;   LOCATION: 169, 181, 265, 269
;   IDENTIFICATION METHOD: Xaa = unknown
US-08-147-592A-11

Query Match         75.4%;  Score 869.6;  DB 3;  Length 1000;
Best Local Similarity 97.5%;  Pred. No. 2.5e-213;
Matches  891;  Mismatches  0;  Conservative  0;  Indels  20;  Gaps  3;

Qy       244 TTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG 303
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Db        87 |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
             TTCTTTTTCTTTAGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTG 146

Qy       304 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCACTTGATG 363
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       147 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCACTTGATG 206

Qy       364 AATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 423
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       207 AATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 266

Qy       424 ATGTTCACCCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTGCACATTGCCGTGTGC 483
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       267 ATGTTCACCCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTGTGC 326

Qy       484 CACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       327 CACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 386

Qy       544 ATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC 603
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       387 ATCTGCCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC 446

Qy       604 AGGGAAGACGTCGATGTCATTGAGTGTCATCGTCTTCCTCAGTTCCCAGATGATGACTACTTCCTGG 663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       447 AGGGAAGGTGTCGATGTCATTGAGTGTCGTTGAGTTCCCAGATGATGACTACTTCCTGG 506

Qy       664 TGGGACCTCTTCATGAAGATCTGCGTCTTCAGCTTTCGTCGCTTGCCTTCGTGTCCTCATC 723
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       507 TGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTCGTCGCTTGCCTTCGTGTCCTCATC 566

Qy       724 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGC 783
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       567 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGANNGTCCGGCTCCTTTCTGGC 626

Qy       784 TCCCGAGAAAGATCGCAACCTGGTAGGATCACCAGACTGGTCTGGTGGTGGCA 843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       627 TCCCGAGAAAGAGATNNCAACCTGCGTAGGATCACCAGACTGGTCTGGTGGTGGCA 686

Qy       844 GTCTTCGTCGTCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCGGGGAGC 903
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       687 GTCTTCGTCGTCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCGGGGAGC 746

Qy       904 ACCTCCCACAGCACAGTCTGCTCTCTCTCCAGTATTACTTCTGCATTGCCTTAGGCTATACC 963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       747 ACCTCCCACAGCACAGTCTGCTCTCTCTCCAGCTATTACTTCTGCATCCGCCTTAGGCTATACC 806

Qy       964 AACAGTAGCGCTGAATCCCATTCTTCTCACGCCCTTCTTGATGAAAACTTCAAGCGCGGTGTTTC 1023
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       807 AACAGTAGCGCTGAATCCCATTCTTCTCACGCCCTTCTTGATGAAAACTTCAAGCGCGGTGTTTC 866

Qy      1024 CGGGACTTCTGCTTTCCACTGAAGATGAGCGGCCAGAGCACTAGCAGAGTCCGA 1083
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       867 CGGGACTTCTGCTTTCCACTGAAGATGAGCGGCCGCNAGAGCACTAGCAGAGTCCGA 926

Qy      1084 AATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATG---GATGAATAAACCAGTA 1140
             |||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db       927 AATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATGATGAATAAACCAGTA 986

Qy      1141 TGACTAGTCGTGGA 1154
             |||||||||||||
Db       987 TGACTAGTCGTGGA 1000


RESULT 12
US-08-292-694A-11
; Sequence 11, Application US/08292694A
; Patent No. 6319686
; GENERAL INFORMATION:
;  APPLICANT: BELL, GRAEME
;  APPLICANT: REISINE, TERRY
;  APPLICANT: YASUDA, KAZUKI
;  TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
```

```
         NUMBER OF SEQUENCES: 46
         CORRESPONDENCE ADDRESS:
            ADDRESSEE: Arnold, White & Durkee
            STREET: P. O. Box 4433
            CITY: Houston
            STATE: Texas
            COUNTRY: USA
            ZIP: 77210
         COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
            SOFTWARE: PatentIn Release #1.0, Version #1.25
         CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/08/292,694A
            FILING DATE: August 19, 1994
            CLASSIFICATION: 435
         PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/066,296
            FILING DATE: 20 May 1993
            CLASSIFICATION: 435
            APPLICATION NUMBER: 08/100,694
            FILING DATE: 30 July, 1993
            CLASSIFICATION: 435
            APPLICATION NUMBER: 08/147,592
            FILING DATE: 5 No. 6319686ember 1993
            CLASSIFICATION: 435
            APPLICATION NUMBER: PCT/US94/05747
            FILING DATE: 20 May 1994
            CLASSIFICATION: 435
         ATTORNEY/AGENT INFORMATION:
            NAME: MARK B. WILSON
            REGISTRATION NUMBER: 37,259
         REFERENCE/DOCKET NUMBER: ARCD:140/WIM
         TELECOMMUNICATION INFORMATION:
            TELEPHONE: (512) 418-3000
            TELEFAX: (713) 789-2679
            TELEX: 79-0924
         INFORMATION FOR SEQ ID NO: 11:
         SEQUENCE CHARACTERISTICS:
            LENGTH: 1000 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
         MOLECULE TYPE: DNA (genomic)
         FEATURE:
            NAME/KEY: N
            LOCATION: 607-608, 642-643, 896, 906
            IDENTIFICATION METHOD: N = A, C, G or T
         FEATURE:
            NAME/KEY: CDS
            LOCATION: 102..986
         FEATURE:
            NAME/KEY: Xaa
            LOCATION: 169, 181, 265, 269
            IDENTIFICATION METHOD: Xaa = unknown
US-08-292-694A-11

Query Match         75.4%;  Score 869.2;  DB 3;  Length 1000;
Best Local Similarity 97.5%;  Pred. No. 2.5e-213;
Matches  891;  Conservative  0;  Mismatches  20;  Indels  3;  Gaps  1;

Qy   244 TTCGTGATCATCCGATACACAAAGATGAAGACAGCAACACATTTACATATTTAACCTG 303
             |||||  ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    87 TTCTTTTCTTTTAGATACACAAAGATGAAGACAGCAACACATTTACATATTTAACCTG 146

Qy   304 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 206

Qy   364 AATTCCTGGCCTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 423
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 AATTCCTGGCCTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 266
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Qy   424 ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGC 483
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   267 ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGC 326

Qy   484 CACCCGTGAAGGTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 543
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327 CACCCGTGAAGGTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 386

Qy   544 ATCTGGCTGCTGTCGTCATCTGTGGCATCTCGCAATAGTCCTTGGAGGCACCAAAGTC 603
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   387 ATCTGGCTGCTGTCGTCATCTGTGGCATCTCGCAATAGTCCTTGGAGGCACCAAAGTC 446

Qy   604 AGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTCTGCCCGAGTGACTACTCCTG 663
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   447 AGGGAAGTGTCGATGTCATTGAGTGCTGCTTGCAGTCTGCCCGAGTGACTACTCCTG 506

Qy   664 TGGGACCCTTCATGAAGATCTGGCTTCATCTTGCCTTCGTGATCCCTGTCCTCATC 723
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   507 TGGGACCCTTCATGAAGATCTGGCTTCATCTTGCCTTCGTGATCCCTGTCCTCATC 566

Qy   724 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCTCGGC 783
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   567 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGNGTCCGGCTCCTTCTCGGC 626

Qy   784 TCCCGAGAGAAAGATCGCAACTGCGTAGGATCACCAGACTGGTCCTGCTGGTGGTGGCA 843
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   627 TCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTCCTGCTGGTGGTGGCA 686

Qy   844 GTCTTCGTCGTCTGCTGGACTCCCATTCCATTCAGCTATTACTTCTGCATTGCTTAGCC 903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   687 GTCTTCGTCGTCTGCTGGACTCCCATTCCATTCAGCTATTACTTCTGCATTGCTTAGCC 746

Qy   904 ACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACC 963
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   747 ACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACC 806

Qy   964 AACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTC 1023
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   807 AACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTC 866

Qy  1024 CGGGACTTCTGCTTCCACTGAAGATGAGGATGGCGGCAGAGCACTAGCAGAGTCCGA 1083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   867 CGGGACTTCTGCTTCCACTGAAGATGAGGATGGCGGCAGAGCACTAGCAGAGTCCGA 926

Qy  1084 AATACAGTTCAGGATCCTGCTTACCTGGAGGGACATCGATGG---GATGAATAAACCAGTA 1140
             ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db   927 AATACAGTTCAGGATCCTGCTTACCTGGAGGGATGGGATGATGAATAAACCAGTA 986

Qy  1141 TGACTAGTCGTGGA 1154
             ||||||||||||||
Db   987 TGACTAGTCGTGGA 1000
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RESULT 13
US-08-430-286A-1
;  Sequence 1, Application US/08430286A
;  Patent No. 6225080
;  GENERAL INFORMATION:
;     APPLICANT: Uhl, George R.
;     APPLICANT: Eppler, C. Mark
;     APPLICANT: Wang, Jai-Bel
;     TITLE OF INVENTION: Mu-Subtype Opioid Receptor
;     NUMBER OF SEQUENCES: 14
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Darby & Darby PC
;        STREET: 805 Third Avenue
;        CITY: New York
;        STATE: New York
;        COUNTRY: US
;        ZIP: 10022
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
```

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          COMPUTER:  IBM PC compatible
          OPERATING SYSTEM:  PC-DOS/MS-DOS
          SOFTWARE:  PatentIn Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER:  US/08/430,286A
          FILING DATE:  28-APR-1995
          CLASSIFICATION:  536
     ATTORNEY/AGENT INFORMATION:
          NAME:  Robinson, Joseph R.
          REGISTRATION NUMBER:  33,448
          REFERENCE/DOCKET NUMBER:  0646/1A843-US5
     TELECOMMUNICATION INFORMATION:
          TELEPHONE:  212-527-7700
          TELEFAX:  212-753-6237
          TELEX:  236687
     INFORMATION FOR SEQ ID NO: 1:
     SEQUENCE CHARACTERISTICS:
          LENGTH:  2135 base pairs
          TYPE:  nucleic acid
          STRANDEDNESS:  single
          TOPOLOGY:  linear
     MOLECULE TYPE:  cDNA to mRNA
     ORIGINAL SOURCE:
          ORGANISM:  Rattus rattus
     IMMEDIATE SOURCE:
          CLONE:  mu receptor cDNA
US-08-430-286A-1

Query Match         39.0%;  Score 449.6;  DB 3;  Length 2135;
Best Local Similarity   67.1%;  Pred. No. 2.4e-105;
Matches  670;  Conservative   0;  Mismatches 319;  Indels   9;  Gaps    2;

Qy   110 ACAGCAACGGCAGCGCCCGGCTCGGAGGACGGCGAGCTGGAGCCGCACATCTCCCCGG 169
             || || ||| | |||| | ||||| || || || | | || || |  |||| ||||
Db   167 ACCGCACCGGGCTTGGCGGGAACGACACAGCCTGTGCCCTCAGACGGCAGCCCTTCCATGG 226

Qy   170 CCATCCGGTCATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCTGTGGGCTTGGGTGGGCA 229
             || |||| ||| ||| || || ||| || || |||| || |||||| || |||
Db   227 TCACAGCCATTACCATCATGCGCCCTCTATCCTACTTTGTGTGTGTAGTGGGCCTCTTCGGAA 286

Qy   230 ACTCGCTGGTCATGTTCGTGATCATCCGATACACAAAGATGAAGCAGCAACCAACATTT 289
             || || ||||| ||| ||| ||| |||| |||||| |  || ||| | |||||
Db   287 ACTTCCTGGTCATGTATGTGATTGTAAGATACACCAAAAATGAAGACTGCCACCAACATCT 346

Qy   290 ACATATTTAACCTGGCTTGGCAGATGCTTTAGTTACTACAACCGTCCCTTTCAGAGTA 349
             |||| || ||||| || ||| | || || ||| || || || || ||||||||||
Db   347 ACATTTTCAACCTTGCTCTGGCAGACGCCTTAGCGACCACTGCACTCGCCCTTTCAGAGTG 406

Qy   350 CGGTCTACTTGATGAATTCCTGGCCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCAA 409
             |||||| || |||| || ||||| || |||||| || |||| ||| || || |||||
Db   407 TCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCCTCGGAACATCGTGATCTCAA 466

Qy   410 TTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATGAGCGTGACCGCT 469
             || ||| | ||||| |||| ||||| || || |||| |||||| || || |||||
Db   467 TAGATTACTACAACATGTTCACCAGCATATTCACCCTCTGCACCATGAGCGTGACCGCT 526

Qy   470 ACATTGCCCGTGCCACCCGTGAAGGCTTTGGACTTCCGGCCACACCCCTTGAAGGCCAAAGA 529
             || |||||||| ||||||| ||||| || ||||||| ||||| ||||| |||||| ||||
Db   527 ACATTGCTGTCTGCCACCAGTCAAAGCCCTGGATTTCCGTACCCCCGAAATGCCAAAA 586

Qy   530 TCATCAAATATCTGCATCTGGCTGCTGTGTCATCGTTGGCATCTCTGCAATAGTCCTTG 589
             |||||| ||  ||||| | || || ||| || || |||| |||| || || || |||
Db   587 TCGTCAACGTCTGCAACTGGACATGATCCTCTCTTCTGCGCCTGTAATGTTCATGG 646

Qy   590 GAGGCACCAAAGTCAGGGAAGACGTCGATGCTCATTGAGTGCTCCTTGCAGTTCCCAGATG 649
             |||| | || ||| | ||| || |||| |||    ||| | ||| |||| || || ||
Db   647 CAACCACAAAATACAGGCAGCAGGGGTC------CATAGATTGCACCCTCACCTTCTCCCACC 700

Qy   650 ATGACTACTCCTGTGGGACCTCTTCATGCAAGAATCGGCTTCATCTTTGCCTTCGTGA 709
             ||| || || |||| ||| ||| || |  || || ||||  |||| |||| || |||
Db   701 CAACCTGGTACTGGGAGAACCTGCTC---AAAATCTGTGTCTTATCTTCGCTTTCATCA 757

Qy   710 TCCCTGTCCTCATCATCACCGTCTGCTACACCCTCGATGATCCCTGAGCTGTCCAAGAGCGTCC 769
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Db   758 TGCCGGTCCTCATCACTGTGTGTTACGGCCTGATGATCTTACGACTCAAGAGCGTTC 817
             ||| ||||||||||| || || || |||| || ||||| ||| || ||||| |||
Qy   770 GGCTCCTTTCGGCTCCCGAGAGAAAGATGCAACCTGCTGGAGATCCGGGTAGGACTCGGTCC 829
             | || |||  || || |||| ||||  ||| | | |||| ||| |  || || ||
Db   818 GCATGCTATCGGCGGCTCCAAAGAAAAGGACAGGAATCTGCGCGAGATCTCGGGATGGTGC 877
             | || ||| | ||| ||| | |||| || |||| || || |||| || || ||
Qy   830 TGGTGGTGGTGGCAGTCTTCGTCTGGACTCCCATTCACATATTCATCCTTGGTGG 889
             ||| || || |||| || ||| ||| || || ||| |||| || ||||| ||
Db   878 TGGTGGTCGTGGCTGTGATTTATGTCTGCTGGAGACCCCCATCCACATCACGTCATCATCA 937
             | || || ||||| || || || || || |||| |||| || ||| ||||||
Qy   890 AGGCTCTGGGGAGCACCTCCACAGCACAGCTGCTCCTTCCAGCTATTACTTCTCCGTCATTG 949
             ||||||||||| | |||| || || || ||||| || ||||| || ||  || |||||
Db   938 AAGGCTGATCACGATTCCAGAAACCACATTTCAGACCGGTTCCTGCCACTTCTGCATTG 997
             |||| || || || |  ||| || || ||||| || || ||| ||| |||||||
Qy   950 CCTTAGGCTATACAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACT 1009
             || ||||| || || || |||| |||| || ||||| ||| || ||||| |||||||
Db   998 CTTTGGGTTACACGAACAGCTGCCTGAATCCCATTCTTTACGCCTTTCTGGATGAAAACT 1057
             || |||||| |||| || ||||| |||||| ||||| || ||| ||||| |||||||
Qy  1010 TCAAGCGGTGTTTTCGGGACTTCTGCTTTCCACTGAAGATGAGATGACGGGCAGAGCA 1069
             ||||| ||| || ||||| ||||| |||| || ||| ||| || || || |||| |
Db  1058 TCAAGCGATGTTCAGAGAGTTCTGCATCCCCAACCTCGTCCACGATCGAACAGCAAAACT 1117
             ||||| || |||| ||| |||||| | ||| || || || ||| || |||| |||||||
Qy  1070 CTAGCAGAGTCCGAAATACAGTTCAGGAGATCCTGCTTAC 1107
             ||| ||  | ||| ||| | |||| ||| || ||| |||
Db  1118 CCACTCGAGTCCGTCAGACACTAGGGAACATCCCTCC 1155
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RESULT 14
US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;   APPLICANT: Yu, Lei
;   TITLE OF INVENTION: Mu Opioid Receptors: Compostions and Methods
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/889,108
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/305,518
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: INDA005\WIM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1618 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (cDNA)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 214..1410
; US-08-889-108-1
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RESULT 15
US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;    APPLICANT:   Yu, Lei
;    TITLE OF INVENTION:   Mu Opioid Receptors: Compostions and Methods
;    NUMBER OF SEQUENCES:   17
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Arnold, White & Durkee
;       STREET:  P. O. Box 4433
;       CITY:  Houston
;       STATE:  TX
;       COUNTRY:  USA
;       ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/889,108
;       FILING DATE:
;       CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/305,518
;       FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Wilson, Mark B.
;       REGISTRATION NUMBER:  37,259
;       REFERENCE/DOCKET NUMBER:  INDA005\WIM
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  512-418-3000
;       TELEFAX:  512-474-7577
; INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  1618 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
;    FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  339..1235
;
US-08-889-108-3

Query Match      38.8%;  Score 448;  DB 3;  Length 1618;
Best Local Similarity  67.0%;  Pred. No. 5.4e-105;
Matches  669;  Conservative  0;  Mismatches 320;  Indels  9;  Gaps  2;

Qy   110  ACAGCAACGGCAGCGCCGGCTCCGGAGGACGCGCAGCTGAGCCCGCGACATCTCCCCG  169
          || ||||  |||| | | |||  |||| |||  | | |  ||||  ||||||| |||
Db   350  ACCGCACCGGCGCTTGGCGGGGAACGACAGCCTGCCCTCGTGGGCTTGGTGTGGCA    409

Qy   170  CCATCCCGGTCATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGAGTGGTGGGCA  229
          |||    | |  | |  ||| |  || | || || || | || |||| || || ||||
Db   410  TCACAGCCATTACCATCATCATGGCCCTCTACTCTACTCTGTGTGTGTAGTGAGCTTCGGAA  469

Qy   230  ACTCGCTGGTCATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTT  289
          ||||| || ||||||||||||||||  || || | | ||||||  |||||||  ||||||
Db   470  ACTTCCTGGTCATGTATGTGATTGTGATGTGTAAGATACACACCAAAAATGAAAATCT  529

Qy   290  ACATATTAACCTGGCTTTAGTTACTACAACACATGCCCTTTCAGAGTA  349
          ||| |||||| ||| ||| |  || |||| || || |||||||||||
Db   530  ACATTTTCAACCTTGCTCTGGCAGACGCGCCTTAGCGCAGTACACTGCCCTTTCAGAGTG  589

Qy   350  CGGTCTACTTGATGAATTCCTGGCCTTTGGGGATGTGCGTGCAAGATAGTAATTTCCA  409
          |||||||| | ||| |  |||| |  |||  ||||||| ||| |||| || |||  ||
Db   590  TCAACTACCTGATGGGAACATGGCCCTTCGGGAACCATCCTCTGCAAGATCGTGATCTCAA  649

Qy   410  TTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCT  469
          ||||||||||||||||||||| ||||| ||| ||  |  | |||  |||  |||||| |
Db   650  TAGATTACTACAACATGTTCACCAGCATATTCAACCCTCTGCACCATGTGGACCGCGCT  709

Qy   470  ACATTGCGTGTGCCACCCGTGAAGGCTTGACTTCCGCACACCCTTGAAGGCAAAGA  529
          ||| | ||||| |||| |  || |||||  | ||||  |||   | ||  |||||
Db   710  ACATTGTGTCTGCGCCAACCCAGTCAAAGCCCTGAATTCCGTACCCCCGAAATGCCAAAA  769

Qy   530  TCATCAATATCTGCATCTGGCTGTCCGTGCTCTCTGTTGGCATCTCTGCAATAGTCCTTG  589
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Db   770  TCGTCAACTGTCGACATCTGCATCTGGCTCTGCCATCGGTGTAAGTTCATGG  829

Qy   590  GAGGCACCAAAGTCAGGGAAGACGTCGATGTGCAGTCCCAGTGATG  649
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Qy   650  ATGACTACTCCTGGTGGGAACCTGTTCTTCATCTTTTCGTTTTCATCA  709
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Qy   710  TCCCGTGTCCTCATCATCATCATCGTCGTCTCACACCCTGATGATCCTGCGTCTCAAGAGGCTCC  769
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Qy   770  GGCTCCTTCTGGCTCCCCGAGAGAAAGAATCGCAACCTGCGTAGGATCACCGACTGTTCC  829
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Db   1001 GCATGCTATCGGGCTCCCTCAAAGAAGAAAGAGACAGGAATCTGCGCGACTCCGGATGGTGC  1060

Qy   830  TGGTGGTTGGTGGTCGTGGCTGTATTATCGTCTGCGACCCCACCATCACGTCATCATCA  889
          || ||||| ||| | | ||||  |   |  |   || ||  | |||  | | ||||||
Db   1061 TGGTGGTCGTGTGGCTGTTATCGTCTGCTGGACCCCCATCACCACACGCTATTACTTTGCAGTC  1120

Qy   890  AGGCTTCTGGGGAGCACCTCCCACAGCACAGCTGTTCCTCCAGCTATTACTTCTGCATTG  949
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Db   1121 AAGCGCTGATCACGACGTTCCACAGCTTCCAGAACATTTCAGACACTTCCTGCTCTGCATTG  1180

Qy   950  CCTTAGGCTATACCAACAGTAGCCTGAATTCCTACCGCCTTCCATTCTTCTTGATGAAAACT  1009
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Db   1181 CTTTGGGTTACGACAGTGCTCCTGAATCCAGTTCTTTACGCCCTTCCGTGATGAAAACT  1240

Qy   1010 TCAAGCCGGTGTTTCCGGGACTTCTGCTTGCTGTATTATCGTCATCCCAACCTCGTGCAGCA  1069
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Db   1241 TCAAGCAGATGCTTCAACAGAGTGCTTCAATCCCAACCTCGTTCGCAGCGCAGACA  1300

Qy   1070 CTAGGAGTCGGAAATACAGTTCAGGATCCTGCTTAC  1107
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Db   1301 CCACTCCAGTCGCTGGGGAACACACTAGGGAACATCCCCTCC  1338

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Thu Apr 7 08:55:55 2005

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Db   650 TAGATTACTACAACATGTTCACCAGCATATTCACCCCTCTGCACCATGAGCGTGGACCGCT  709

Qy   470 ACATTGCCGTGCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGA        529
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Db   710 ACATTGCTGTCTGCACCCAGTCAAAGCCCTGGATTTCCGTACCCCCCGAAATGCCAAAA    769

Qy   530 TCATCAATATCTGCATCTGCCTGCGTCGTGCATCTGTTGGCATCTCTGCAATAGTCCTTG   589
         ||| |||| ||||| || | | ||||| | || || |||||| ||||| |||| | ||
Db   770 TCGTCAACGTCTGCAACTCGGATCCTCTCTTCTGCCATCGGTCTGCCTGTAATGTTCATGG  829

Qy   590 GAGGCACCAAAGTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCGAGTTCCCAGATG  649
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Db   830 CAACCACAAAATACAGGCAGGGGTC------CATAGATTGCACCCTCACGTTCTCCCACC    883

Qy   650 ATGACTACTTCCTGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGA  709
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Qy   710 TCCCTGTCCTCATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCC   769
         | || || |||||||| || |||  |   |||||||||||  | ||  ||||||||| |
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Qy   770 GGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCC   829
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Db  1001 GCATGCTATCGCCTCCAAAGAAAAGGACAGAATCTGCCGAGGATCTCGCCGGATGGTGC   1060

Qy   830 TGGTGGTGGTGGCAGTCTTCGTCGTGCTCGGGACTCCCATTCACATATTCATCCTGGTGG   889
         |||||| ||||| || | |  || ||| ||| |  || ||||| || ||| || |||
Db  1061 TGGTGGTCGTGGCTGTGATTTATCGTCGCTGGACCCCATCCCATCTACGTCATCATCA    1120

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Qy   950 CCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCTTCACGGCCTTTCTTGATGAAAACT  1009
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Db  1241 TCAAGGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCCACGATCCAGCAGCAAAACT  1300

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Search completed: April 6, 2005, 12:39:41
Job time : 218 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 766.333 Seconds
(without alignments)
9125.590 Million cell updates/sec

Title: US-09-904-584-3
Perfect score: 1154
Sequence: 1 atggactcccgatccagat........ccagtatgactagtcgtgga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1154	100.0	1154	11	US-09-904-584-3	Sequence 3, Appli
2	1152.4	99.9	1154	11	US-09-904-584-1	Sequence 1, Appli
3	1152.4	99.9	1602	19	US-10-278-698-45	Sequence 45, Appl
4	1152.4	99.9	1602	19	US-10-278-698-559	Sequence 559, App
5	1150.8	99.7	1154	11	US-09-904-584-2	Sequence 2, Appli
6	1150.8	99.7	1154	11	US-09-904-584-4	Sequence 4, Appli
7	1150.8	99.7	1154	11	US-09-904-584-5	Sequence 5, Appli
8	1150.8	99.7	1154	11	US-09-904-584-6	Sequence 6, Appli
9	1150.8	99.7	1154	11	US-09-904-584-7	Sequence 7, Appli
10	1144.4	99.2	1182	15	US-10-225-567A-147	Sequence 147, App
11	1144.4	99.2	1182	15	US-10-345-680-19	Sequence 19, Appl
12	1144.4	99.2	1182	17	US-10-305-720-1417	Sequence 1417, Ap
13	1144.4	99.2	1182	18	US-10-283-975A-80	Sequence 80, Appl
14	1141.6	98.9	1143	16	US-10-318-661-1	Sequence 1, Appli
15	1136.2	98.5	1284	16	US-10-318-661-3	Sequence 3, Appli
16	1133.4	98.2	1143	15	US-10-345-680-21	Sequence 21, Appl
17	1130.2	97.9	1143	10	US-09-826-509-542	Sequence 542, App
18	1130.2	97.9	1143	19	US-10-925-095-542	Sequence 542, App
19	999.4	86.6	1275	16	US-10-318-661-5	Sequence 5, Appli
20	994.6	86.2	1275	16	US-10-318-661-7	Sequence 7, Appli
21	979.4	84.9	1875	16	US-10-318-661-13	Sequence 13, Appl
22	963.4	83.5	1875	16	US-10-318-661-15	Sequence 15, Appl
23	912.4	79.1	1408	9	US-09-214-904-5	Sequence 5, Appl
24	877.8	76.1	1911	16	US-10-318-661-17	Sequence 17, Appl
c	25	469	40.6	585	13	US-10-027-632-188121	Sequence 188121,
c	26	469	40.6	585	13	US-10-027-632-188122	Sequence 188122,
c	27	469	40.6	585	17	US-10-027-632-188121	Sequence 188121,
c	28	448	38.8	585	17	US-10-027-632-188122	Sequence 188122,
29	448	38.8	1618	10	US-09-841-720-1	Sequence 1, Appli
30	448	38.8	1618	10	US-09-841-720-3	Sequence 3, Appli
31	437.8	37.9	1464	14	US-10-185-083-25	Sequence 25, Appl
32	436.4	37.8	1239	14	US-10-080-917-10	Sequence 10, Appl
33	436.4	37.8	1245	14	US-10-080-917-8	Sequence 8, Appli
34	436.4	37.8	1388	14	US-10-185-083-26	Sequence 26, Appl
35	436.4	37.8	1431	14	US-10-080-917-6	Sequence 6, Appli
36	436.4	37.8	2149	14	US-10-080-917-12	Sequence 12, Appl
37	436.4	37.8	2162	11	US-09-883-839-1	Sequence 1, Appli
38	436.4	37.8	2162	11	US-09-883-839-3	Sequence 3, Appli
39	436.4	37.8	2162	11	US-09-883-839-5	Sequence 5, Appli
40	436.4	37.8	2162	15	US-10-225-567A-185	Sequence 185, App
41	436.4	37.8	2162	17	US-10-305-720-1379	Sequence 1379, Ap
42	436.4	37.8	2279	19	US-10-477-714-33	Sequence 33, Appl
43	434.8	37.7	1176	10	US-09-935-061-11	Sequence 11, Appl
44	434.8	37.7	1176	18	US-10-692-071-11	Sequence 11, Appl
45	434.8	37.7	1473	14	US-10-080-917-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-904-584-3
; Sequence 3, Application US/09904584
; Publication No. US2004009704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-3

Query Match   100.0%; Score 1154; DB 11; Length 1154;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1154; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGACCCTACCTGCGCCCCGAGCGCC 60
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Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGACCCTACCTGCGCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCCAACAGCAGCGGCCGCCTGGTTTCCCGGCTGCGGCCCGACAGCAACGGC 120
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RESULT 2
US-09-904-584-1

; Sequence 1, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-1

Query Match   99.9%;   Score 1152.4;   DB 11;   Length 1154;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1153;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   0;

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Qy       1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCCGGCCCCTCGCGCCCCGAGCGCC   60
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Qy      61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCGCCGACAGCAGCAACGGC  120
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Qy     121 AGCGGCCGGCTCGGAGGACGGCGCAGCTCGGAGCCCGCACATCTCCCGGCCATCCCGGTC  180
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Qy     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTCGTTGGTGGGCAACTCGCTGGTC  240
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Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCACATTTACATATTTAAC  300
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Qy     481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Db     121 AGCGGCCGGCTCGGAGGACGGCGCAGCTCGGAGCCCGCACATCTCCCGGCCATCCCGGTC  180

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Qy     841 GCAGTCTTCTCGTCGTCTGCTGGATCTCCATTCATCCTGTGGAGGCTCTCGGGG  900
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Db     841 GCAGTCTTCTCGTCGTCTGCTGGATCTCCATTCATCCTGTGGAGGCTCTCGGGG  900

Qy     901 AGCACCTCCACAGACACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AGCACCTCCACAGACACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960

Qy     961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy    1021 TTCCGGGACTTCTGCTTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTCCGGGACTTCTGCTTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGCCTTACCTGAGGGAACATCCATGGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGCCTTACCTGAGGGAACATCCATGGAATAAACCAGTA 1140

Qy    1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db    1141 TGACTAGTCGTGGA 1154
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Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy    721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy    841 GCAGTCTTCGTGCGTCGTCCGGAGGCTCGGGG 900
          ||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTGCGTCGTCCGGAGGCTCGGGG 900

Qy    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCACTTCGCCTTCGGCTTT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCACTTCGCCTTCGGCTTT 960

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGGATGGAGGCGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGAGGATGGAGGCGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCTTCGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCTTCGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154


RESULT 3
US-10-278-698-45
; Sequence 45, Application US/10278698
; Publication No. US2005003734A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-45

  Query Match        99.9%;  Score 1152.4;  DB 19;  Length 1602;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1153;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  0;

Qy      1 ATGGACTCCCCGATCCAGATCTTCCGCGGGAGCCCGGGCCCTGGTTCCCGCGGACCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 ATGGACTCCCCAACAGCTTCCGGGGAGCCCTACCTGGGCCCGGGCCCGACCGCC 435

Qy     61 TGCCTGCCCCCAACAGCAGCGCGCTGGAGCCCGGGTTCCCGGGCCTGGGCCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 TGCCTGCCCCCAACAGCAGCGCGCTGGAGCCCGGGTTCCCGGGCCTGGGCCCGACAGCAACGGC 495

Qy    121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGCCGACATCCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGCCGACATCCCCGGCCATCCCGGTC 555
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Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTGGGGCTTGGTGGGCAACTCGCTCGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTGGGGCTTGGTGGGCAACTCGCTCGGTC 615

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db    616 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAC 675

Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 735

Qy    361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTCGAAGTAGTAATTCCATTGATTACTAC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 ATGAATTCCTGGCCTTTTGGGATGTGCTGTCGAAGTAGTAATTCCATTGATTACTAC 795

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACATCGATGAGCGTGACCGCTACATGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 AACATGTTCACCAGCATCTTCACCTTGACATCGATGAGCGTGACCGCTACATGCCGTG 855

Qy    481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 915

Qy    541 TGATCTGGCTGCGTCGTCATCGTCGTGATGAGTCCTTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 TGATCTGGCTGCGTCGTCATCGTCGTGATGAGTCCTTGCAATAGTCCTTGGAGGCACCAAA 975

Qy    601 GTCAGGGAAGACGTGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 GTCAGGGAAGACGTGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 1035

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 1095

Qy    721 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 1155

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 1215

Qy    841 GCAGTCTTCGTGCGTCGTCCATTCACATATTCACATATTCATCCTGGTGGTGCGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCAGTCTTCGTGCGTCGTCCATTCACATATTCACATATTCATCCTGGTGGTGCGGG 1275

Qy    901 AGCACCTCCCACAGCACAGCTCCCATTCTCTCCCAGCTATTGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AGCACCTCCCACAGCACAGCTCCCATTCTCTCCCAGCTATTGCCTTAGGCTAT 1335

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 ACCAACAGTAGCCTGAATCCCATTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC 1395

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGACATCGATGGGATGAATAAACCAGTA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGACATCGATGGGATGAATAAACCAGTA 1455

Qy   1081 CGAAATACAGTTCAGGATCTTCGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CGAAATACAGTTCAGGATCTTCGAGGGACATCGATGGGATGAATAAACCAGTA 1515

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1516 TGACTAGTCGTGGA 1529


RESULT 4
US-10-278-698-559
; Sequence 559, Application US/10278698
```

; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 03027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-559

Query Match   99.9%;   Score 1152.4;   DB 19;   Length 1602;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 1153;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1   ATGGACTCCCCGATCCAGATCTTCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 ATGGACTCCCCGATCCAGATCTTCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   435

Qy   61   TGCCTGCCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGAGCCCGACAGCAGCAACGC   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 TGCCTGCCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGAGCCCGACAGCAGCAACGC   495

Qy   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCTGGACTGGACCCGCACATCTCCCCGGCCATCCCCGGTC   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCTGGACTGGACCCGCACATCTCCCCGGCCATCCCCGGTC   555

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCAACTCGCTGGTC   240
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGCAACTCGCTGGTC   615

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTTACATATTTAAC   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTTACATATTTAAC   675

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTCACTTG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTCACTTG   735

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   736 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   795

Qy   421 AACACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   796 AACACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG   855

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   856 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC   915

Qy   541 TGCATCTGGCTGTCGTCGATCTCATCGTTGGCATCTCTGCAATAGTCCTTGCAGAGGCACCAAA   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   916 TGCATCTGGCTGTCGTCGATCTCATCGTTGGCATCTCTGCAATAGTCCTTGCAGAGGCACCAAA   975

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   976 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   1035

Qy   661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTGATCCCTGTCCTC   720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTGATCCCTGTCCTC   1095

Qy   721 ATCATCATCGTCTGCTACACCCTGCTCTCAAGAGCGTCCGGCTCCTTTCT   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 ATCATCATCGTCTGCTACACCCTGCTCTCAAGAGCGTCCGGCTCCTTTCT   1155

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTCGTG   840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG   1215

Qy   841 GCAGTCTTCGTCGTCTGCTGGGACTCCCATTCACATATTCACATATTCATCCTCGGTGTGGAGGGCTCTGGGG   900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCAGTCTTCGTCGTCTGCTGGGACTCCCATTCACATATTCACATATTCATCCTCGGTGTGGAGGGCTCTGGGG   1275

Qy   901 AGCAACTCCCACAGCACAGTGCTCTCTCCCAGCTATTACTTCTGCATGCCTTAGGCTAT   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AGCAACTCCCACAGCACAGTGCTCTCTCCCAGCTATTACTTCTGCATGCCTTAGGCTAT   1335

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT   1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 ACCAACAGTAGCCTGAATCCCATTCCTACGCCTTTCTTGATGAAAACTTCAAGCGCGTGT   1395

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCCAGAGCACTAGCAGAGTC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCCAGAGCACTAGCAGAGTC   1455

Qy   1081 CGAAATACAGTTCAGGATCCGCTACCTGAGGACATCGATGGGATGAATAAACCAGTA   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CGAAATACAGTTCAGGATCCGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTA   1515

Qy   1141 TGACTAGTCGTGGA   1154
           ||||||||||||||
Db   1516 TGACTAGTCGTGGA   1529

RESULT 5
US-09-904-584-2
; Sequence 2, Application US/09904584
; Publication No. US2004009770441
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1152;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1   ATGGACTCCCCGATCCAGATCTTCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   ATGGACTCCCCGATCCAGATCTTCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60

Qy   61   TGCCTGCCCCCCAACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCAACGGC   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   TGCCTGCCCCCCAACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAGCAACGGC   120

Qy   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCTGGACCACATCTCCCCGGCCATCCCCGGTC   180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGGCGCAGCTGGAGCTGGACCACATCTCCCCGGCCATCCCCGGTC   180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGGGCAACTCGCTGGTC   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGGGCAACTCGCTGGTC   240

```
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 1154
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-904-584-4

Query Match               99.7%;     Score 1150.8;     DB 11;   Length 1154;
Best Local Similarity      99.8%;     Pred. No. 0;
Matches 1152;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   0;
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Qy      1 ATGGACTCCCGATCCAGATCTTCCGGCGGGGGAGCCGGCCCTACCTGCCGCCCGAGCGGC    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCAGATCTTCCGGCGGGGGAGCCGGCCCTACCTGCCGCCCGAGCGGC    60

Qy     61 TGCCTGCCCCCAACAGCAGCGGCCGCCTGGTTCCCGGCTGGAGCCGAGCCGGCAACAGCGC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGGCCGCCTGGTTCCCGGCTGGAGCCGAGCCGGCAACAGCGC   120

Qy    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGACCTCCCGGCCATCCGGTC   180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGACCTCCCGGCCATCCGGTC   180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTGTCGTGGGGCAACTGCTGCGGTC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTGTCGTGGGGCAACTGCTGCGGTC   240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC   300

Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG   360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCAAGATAGTAATTTCCATTGATTACTAC   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGCAAGATAGTAATTTCCATTGATTACTAC   420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGACCGTGCACATTGCCGTG   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGACCGTGCACATTGCCGTG   480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540

Qy    541 TGCATCTGGCTGCTGTCTTCGTGTTGGCATCTTCCTTGGAGGCACCAGTA   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCTTCGTGTTGGCATCTTCCTTGGAGGCACCAAA   600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC   660

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC   720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
.Db   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780

Qy    781 GGCTCCCGAGAAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGTG   840
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Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC   300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC   300

Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG   360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCACTTG   360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCAAGATAGTAATTTCCATTGATTACTAC   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGCAAGATAGTAATTTCCATTGATTACTAC   420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGACCGTGCACATTGCCGTG   480
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCTTGACCGTGACCGTGACCGTGCACATTGCCGTG   480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540

Qy    541 TGCATCTGGCTGCTGTCTTCGTGTTGGCATCTTCCTTGGAGGCACCAGTA   600
          ||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCTTCGTGTTGGCATCTTCCTTGGAGGCACCAAA   600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC   660
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC   660

Qy    661 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC   660

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT   780

Qy    781 GGCTCCCGAGAAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGTG   840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGTG   840

Qy    841 GCAGTCTCGTCGCTGCTGGACTCCCATTCATCCTGGTTGGAGGCTCTGGGG   900
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTCGTCGTGTCTGCTGGACTCCCATTCCATTCATCCTGGTTGGAGGCTCTGGGG   900

Qy    901 AGCACCTCCCAGCACAGCTGCGTCTTGCCTTAGGCTAT   960
          |||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCAGCACAGCTGCTCTTGCCTTAGGCTAT   960

Qy    961 ACCAACAGTAGCCTGAATCCCTTCTCACGGCCTTTCTGATGAAAACTTCAAGCGGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCTTCTCACGGCCTTTCTGATGAAAACTTCAAGCGGTGT  1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCACTAGCAGAGTC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCACTAGCAGAGTC  1080

Qy   1081 CGAAATACAGTTCAGGATCCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141 TGACTAGTCGTGGA  1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA  1154
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RESULT 6
US-09-904-584-4
; Sequence 4, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven

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Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTTCAGCTATTACTTCTCGCATTGCCTTAGGCTAT 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTTCAGCTATTGCCTTAGGCTAT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCCATTCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTTCAGCTATTGCCTTAGGCTAT 900

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTCGCATTGCCTTAGGCGGTGT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTCGCATTGCCTTAGGCGGTGT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGCAGAGCACTAGCAGAGTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCCGCAGAGCACTAGCAGAGTC 1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTA 1140

Qy  1141 TGACTAGTCGTGGA 1154
             ||||||||||||||
Db  1141 TGACTAGTCGTGGA 1154
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RESULT 7
US-09-904-584-5
; Sequence 5, Application US/09904584
; Publication No. US2004097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-5

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1152;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   0;

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Qy     1 ATGGACTCCCCGATCCCAGATCTTCCGCGGGGAGGGCCCGGCCTGGGCCCTACCTGCGCCCCCGAGCGCGCC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCCGATCCCAGATCTTCCGCGGGGAGGGCCCGGCCTGGGCCCTACCTGCGCCCCCGAGCGCGCC 60

Qy    61 TGCCTGCCCCCAACAGCAGCGCGGCCGCCTGGTTTCCCGGCTGGGCCTGGGCCGAGCCCGACAGCAACGGC 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGCGGCCGCCTGGTTTCCCGGCTGGGCCTGGGCCGAGCCCGACAGCAACGGC 120

Qy   121 AGCGCGGCCGGCTCGGAGGACGCGCAGTCGGAGCCCGGCCACATCTCCCCGGCCATCCCGGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCGGCCGGCTCGGAGGACGCGCAGTCGGAGCCCGGCCACATCTCCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCAACTCGCTGGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 CTGGCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTGAGGCAAAGATCATCAATATC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTGAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTGTTGGCAATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTGTTGGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTCATTGAGTCATTGAGAGATCTGCGTCTTCATCTTTGCCTTCATCCTGTCCTC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTCATTGAGTCATTGAGAGATCTGCGTCTTCATCTTTGCCTTCATCCTGTCCTC 660

Qy   661 TGGTGGGACCTTCGTCTTCATGAAGATCTGCGTCTTCATGAAGATCTGCGTCTTCGTGATCCGGTCCGGCTCCTTTCT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTTCGTCTTCATGAAGATCTGCGTCTTCATGAAGATCTGCGTCTTCGTGATCCGGTCCGGCTCCTTTCT 720

Qy   721 ATCATCATCGTCTGCTGCTGATCCCGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTGCTGATCCCGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 900

Qy   901 GGCTCCCGAGAGAAAGATCCGCAACCTGCGTAGGATCCAACCTGGTCCTTGGTGGTGGTG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGCTCCCGAGAGAAAGATCCGCAACCTGCGTAGGATCCAACCTGGTCCTTGGTGGTGGTG 960

Qy   961 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 1020

Qy  1021 GCGAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCGAGTCTTCGTCGTCTGCTGCTGACTCCCATTCACATATTCACATATTCACAATTCATCCTGCGTCTCCTTCT 1080

Qy  1081 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCATTGCTATTGCCTTAGGCTAT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTCATTGCTATTGCCTTAGGCTAT 1140

Qy  1141 TGACTAGTCGTGGA 1154
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Db  1141 TGACTAGTCGTGGA 1154
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RESULT 8
US-09-904-584-6
; Sequence 6, Application US/09904584
; Publication No. US2004097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid

```
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-6

Query Match          99.7%;  Score 1150.8;  DB 11;  Length 1154;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1152;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCCAGATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120

Qy     121 AGGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGCCATCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGCCATCCCGGTC 180

Qy     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy     301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy     361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy     481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACAGTCCTTGGAGGCACCAAA 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACAGTCCTTGGAGGCACCAAA 540

Qy     541 TGCATCTGGCTGTCGTCATCGTTGGCATCTTGCTTCTGCAATGTCCTTGCAATAGTCCTTGCATCTTGGAGCACTACTCC 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCATCTGGCTGTCGTCATCGTTGGCATCTTGCTTCTGCAATGTCCTTGCAATAGTCCTTGCATCTTGGAGCACTACTCC 600

Qy     601 GTCAGGGAAGAGACTGCAGACTGATTCATTGAGTGCTCCTTCAGAGTTCCCAGATGATGACTACTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCAGGGAAGAGACTGCAGACTGATTCATTGAGTGCTCCTTCAGAGTTCCCAGATGATGACTACTCC 660

Qy     661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTTGCGTTCGTCGTGATCCCGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTCTTTGCGTTCGTCGTGATCCCGTCCTC 720

Qy     721 ATCATCATCGTTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGTCCTGCGTCTTCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCATCATCGTTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGTCCTGCGTCTTCT 780

Qy     781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTGG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTGG 840

Qy     841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTCGATTGCCATT 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GCGGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGG 900

Qy     901 AGCACCTCCCAGCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AGCACCTCCCAGCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960

Qy     961 ACCAACAGTAGCCTGAATCCATTCCATTCTCTACGCCCTTCTTGATGAAAACTTCAAGCGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ACCAACAGTAGCCTGAATCCATTCCATTCTCTACGCCCTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy    1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGAGGACGCGGCAGAGCACTAGCAGAGTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGAGCGGGCAGAGCACTAGCAGAGTC 1080

Qy    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGCGACATCGATGGACATCGATGAATAAACCAGTA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGCGACATCGATGGACATCGATGAATAAACCAGTA 1140

Qy    1141 TGACTAGTCGTGGA 1154
           ||| ||| ||||||
Db    1141 TGACTAGTCGTGGA 1154


RESULT 9
US-09-904-584-7
; Sequence 7, Application US/09904584
; Publication No. US2004009770441
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-7

Query Match          99.7%;  Score 1150.8;  DB 11;  Length 1154;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1152;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy       1 ATGGACTCCCGATCCAGATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCCAGATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120

Qy     121 AGGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGCCATCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGCCATCCCGGTC 180

Qy     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy     301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy     361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy     481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACAGTCCTTGGAGGCACCAAA 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACAGTCCTTGGAGGCACCAAA 540

Qy     541 ATGGACTCCCGATCATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGACTCCCGATCATCTTCCGCCGGGGAGCCCTACCTGCCCCGAGCGCC 60

Qy      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCCGGCCGAGCCCGACAGCAACGGC 120

Qy     121 AGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCCGCATCTCCCGGTC 180

Qy     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGCTGGGCAACTCGCTGGTC 240

Qy     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 2292
; SEQ ID NO 147
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-147

Query Match   99.2%;   Score 1144.4;   DB 15;   Length 1182;
Best Local Similarity 99.5%; Pred. No. 0;   Gaps 0;
Matches 1148;   Conservative 0;   Mismatches 6;   Indels 0;

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCTACCTGCGCCCCGAGCGCC   60
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Db   14 ATGAATCCCGATTCAGATCTTCCGCGGGAGCCGGGCCTACCTGCGCCCCGAGCGCC   73

Qy   61 TGCCTGCCCCAACAGCAGCGCCTGGTTTCCCGCGCTGGGCTGGGCCGAGCAGCAACGGC  120
        |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db   74 TGCCTGCCCCAACAGCAGCGCCTGGTTTCCCGCGCTGGGCTGGGCCGAGCCGACAGCAACGGC  133

Qy  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCCGCGCACATCTCCCGGTC  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCCCGCGCACATCTCCCGGTC  193

Qy  181 ATCATCACCGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCCAACTCGCTGGTC  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  194 ATCATCACCGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCCAACTCGCTGGTC  253

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCACATTTACATATTTAAC  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCACATTTACATATTTAAC  313

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTAGGTCTACTTG  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTAGGTCTACTTG  373

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTAC  420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  374 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTAC  433

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  493

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  553

Qy  541 TGCATCTGGCTGCTGTCGTCATCTGTGTCAATAGTCCTTGGAGGCACCAAA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  554 TGCATCTGGCTGCTGTCGTCATCTGTGTCAATAGTCCTTGGAGGCACCAAA  613

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  673

Qy  661 TGGTGGGACCTTCTCATGAAGATCGTGTCTTCATCTTTGCCTTGTCGTCTTCATCTTTGCCTTGTCGTCCTC  720
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Db  674 TGGTGGGACCTTCTCATGAAGATCGTGTCTTCATCTTTGCCTTGTCGTCCTC  733
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RESULT 10
US-10-225-567A-147
; Sequence 147, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

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Db  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTTACATATTTAAC  300

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTAC  420
Db  361 ATGAATTCCTGGCCTTTGGGGATGTCGTGCAAGATAGTAATTCCATTGATTACTAC  420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy  541 TGCATCTGGCTGCTGTCGTCATCTGTGTCAATAGTCCTTGGAGGCACCAAA  600
Db  541 TGCATCTGGCTGCTGTCGTCATCTGTGTCAATAGTCCTTGGAGGCACCAAA  600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy  661 TGGTGGGACCTTCTCGTCTGTCGTTCTTTGCCTTCTCGTCGATCCTGTCCTC  720
Db  661 TGGTGGGACCTTCTCGTCTGTCGTTCTTTGCCTTCTCGTCGATCCTGTCCTC  720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCGCGTCCTCTTTCT  780
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCGCGTCCTCTTTCT  780

Qy  781 GGCTCCCGAGAAAGATGCAACCTGCGTAGAACTGGTCCTGGTGGTG  840
Db  781 GGCTCCCGAGAAAGATGCAACCTGCGTAGAACTGGTCCTGGTGGTG  840

Qy  841 GCAGTTTCTGCGTCTGCTGGACTTCCATTCATCCTGGTGGAGGCTCTGGGG  900
Db  841 GCAGTTTCTGCGTCTGCTGGACTTCCATTCATCCTGGTGGAGGCTCTGGGG  900

Qy  901 AGCACCTCCACAGCAGCTGCCTTCTCTCCAGCTATTACTTCTGCATTGCTTAGGCTAT  960
Db  901 AGCACCTCCACAGCAGCTGCCTTCTCTCCAGCTATTACTTCTGCATTGCTTAGGCTAT  960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
Db  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGCGGAGCACTAGCAGAGTC 1080
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGCGGAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGAATAAACCAGTA 1140
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGAATAAACCAGTA 1140

Qy 1141 TGACTAGTCGTGGA 1154
Db 1141 TGACTAGTCGTGGA 1154
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Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCGCCTACCTGCGCCCCGAGCGCC   60
          ||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCCGCCTACCTGCGCCCCGAGCGCC   73

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGCTGGCTCGGCCGAGCCCAGCAGCAACGGC 120
          |||||||||||||||||||||| ||||||||||||||||||||||||||| |||||||||
Db   74 TGCCTGCCCCCAACAGCAGCGGACGGCCTGGTTCCCGCTGGCTCGGCCGAGCCCGACAGCAACGGC 133

Qy   121 AGGCCGGCTCGGAGGAGCGCAGCTGGACTGGAGCCCGCGCACTTCCCGGCCATCCGGTGT 180
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   134 AGGCCGGCTCGGAGGAGCGACGCTGGAGCCGCGCACTTCCCGGCCATCCGGTGT 193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGTGTTGGGGCAACTCCTGGTC 240
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGTGTTGGGGCAACTCCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 300
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTAGTACTACAACCATGCGTGTGCAAGATAGTAGTTTCATTGATTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTAGTACTACAACCATGCGTGTGCAAGATAGTAGTTTCATTGATTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCGTGTGCAAGTAGTAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCGTGTGCAAGTAGTAGTAATTTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGGACTTCCGACACCCTTGAAGGCAAAGATCATCAATATC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGGACTTCCGACACCCTTGAAGGCAAAGATCATCAATATC 493

Qy   481 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCGTCTGTGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCGTCTGTGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGATTCCTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGATTCCTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGACCTCTTCTCATGAAGATCTGCGGTCTCATCTTTGCCTTCGTGATCCCGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGACCTCTTCTCATGAAGATCTGCGGTCTCATCTTTGCCTTCGTGATCCCGTCCTC 733

Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy   781 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTG 853

Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 913

Qy   901 AGCACCTCCCACAGCACCAGCTGCTCTCTCCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACCAGCTGCTCTCTCCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCCATTCTCTACGCCTTTCTGATGAAAACTTCAAGCGGTGT 1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGCGGCAGAGCACTAGCAGAGTC 1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy 1141 TGACTAGTCGTGA 1154
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Db 1154 TGACTAGTCGTGA 1167

Query Match   99.2%;   Score 1144.4;   DB 15;   Length 1182;
Best Local Similarity   99.5%;
Matches 1148;   Conservative 0;   Mismatches 0;   Indels 6;   Gaps 0;

Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 1141 TGACTAGTCGTGGA 1154
                ||||||||||||||
Db 1154 TGACTAGTCGTGGA 1167

RESULT 12
US-10-305-720-1417
; Sequence 1417, Application US/10305720
; Publication No. US2004010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1417
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g532059
US-10-305-720-1417

  Query Match   99.2%;   Score 1144.4;   DB 17;   Length 1182;
  Best Local Similarity   99.5%;   Pred. No. 0;
  Matches 1148;   Conservative   0;   Mismatches   6;   Indels   6;   Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCCGCCCCGAGCGCC 60
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCTGGCCCTACCTGCCGCCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCGGCTGGGCCGAGCAGCAACGGC 120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCGGCTGGGCCGAGCAGCAACGGC 133

Qy 121 AGGCCGGCTCGGAGGACGGCAGCTGAGCGTCCCCGCGCCATCCCGGTC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db 134 AGGCCGGCTCGGAGGACGGCAGCTGAGCGTCCCCGGCCATCCCGGTC 193

Qy 181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 240
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 313

Qy 301 CTGGCTTGGCAGATGCTTTGGGGAGTGCTTAGTTACTACAACATGCCCTTTCAGAGTAC 360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 314 CTGGCTTGGCAGATGCTTTGGGGAGTGCTTAGTTACTACAACATGCCCTTTCAGAGTAC 373

Qy 361 ATGAATTCCTGGCCGGTCTTTGGGGATGGTCGTGCGAGAGTAATTTCCATTGATTACTAC 420
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 374 ATGAATTCCTGGCCGGTCTTTGGGGATGGTCGTGCGAGAGTAATTTCCATTGATTACTAC 433

Qy 421 AACATGTTCACCAGACATCTTCACCTTGACGCTGGACCGCTACATTGCCGTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 434 AACATGTTCACCAGACATCTTCACCTTGACGCTGGACCGCTACATTGCCGTG 493

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy 541 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 554 TGCATCTGGCTGCTGTCGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTCCAGTTCCAGATGATGACTACTCC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 614 GTCAGGGAAGACGTCGATGTCATTGAGTCCAGTTCCAGATGATGACTACTCC 673

Qy 661 TGGTGGGACCTTCTTCATGAGATCTGCGTCTTCATCTTTGCTTCGTCCTGTCCCTC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 674 TGGTGGGACCTTCTTCATGAGATCTGCGTCTTCATCTTTGCTTCGTCCTGTCCCTC 733

Qy 721 ATCATCATCGTCTGCTACACCCTGACTCCTGCGTCTCAAGAGGGTCCGGCTCCTTTCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 734 ATCATCATCGTCTGCTACACCCTGACTCCTGCGTCTCAAGAGGGCGTCCCGCGCTCCTTTCT 793

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTCGTCCTGGTGGTGGTG 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTCGTCCTGGTGGTGGTG 853

Qy 841 GCAGTCTTCGTGCTGTGCTGGACTCCCATTCACATATTCATCATCCTGTGTGGAGGCTCTGGGG 900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 854 GCGGTTTCGTGCTGTGCTGGACTCCCATTCACATATTCATCATCCTGTGTGGAGGCTCTGGGG 913

Qy 901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy 961 ACCACAGTAGCCTGAATCCCATTCCTCTACGGCCCTTCTTGATGAAAACTTCAAGCGGTGT 1020
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 974 ACCACAGTAGCCTGAATCCCATTCCTCTACGGCCCTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAAGATGGAGCGCAGAGCACTAGCAGAGTC 1080
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1034 TTCCGGGACTTCTGCTTCCACTGAAGATGAAGATGGAGCGCAGAGCACTAGCAGAGTC 1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy 1141 TGACTAGTCGTGGA 1154
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 13
US-10-283-975A-80
; Sequence 80, Application US/10283975A
; Publication No. US2004011079ZA1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-80

  Query Match   99.2%;   Score 1144.4;   DB 18;   Length 1182;
  Best Local Similarity   99.5%;   Pred. No. 0;
  Matches 1148;   Conservative   0;   Mismatches   6;   Indels   6;   Gaps   0;

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Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGCGGATGAATCGATGGGATGAATAAACCAGTA 1153
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Qy   1141 TGACTAGTCGTGA 1154
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Db   1154 TGACTAGTCGTGA 1167
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RESULT 14
US-10-318-661-1
; Sequence 1, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-318-661-1

Query Match   98.9%; Score 1141.4; DB 16; Length 1143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Db   1 ATGGACTCCCGATTCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGGC 60

Qy   61 TGCCTGCCCCCAACAGCAGCCGCCTGGTTCCCGGCTGGTCGGCCGGAGCCGACAGCAACGGC 120
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Qy   121 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCACATCTCCCCGGCCATCCCGGTC 180
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Db   121 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCGCGCACATCTCCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAACATTACATATTTAAC 300
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Qy   301 CTGGCTTTGGCAGATGCTTAGTACTACAACCATGACCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTAGTACTACAACCATGACCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGGGACTTCACCTGCCGTG 480
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Db   421 AACATGTTCACCAGCATCTTCACCTTGGGACTTCACCTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTGAAGGCAAAGATCATCAATATC 540
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Qy   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCACCAAA 553

Qy   541 TGCATCTGGCTGCTGCTGTGCTGTCGTCATCCTGTTGGCATCTCTGCAATAGTCCTTGGAGCGCACCAAA 613
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Db   554 TGCATCTGGCTGCTGCTGTGCTGTCGTCATCCTGTTGGCATCTCTGCAATAGTCCTTGGAGCGCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGCTCATTGAGTGCTCCTTGGAGTTCCCAGATGACTACTCC 660
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Qy   661 TGGTGGGACCTCTTCGTCGTCTTCATGTCGTCTTCGTGATCCCGTCCTC 720
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Best Local Similarity 99.7%;   Pred. No. 0;
Matches 1138;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

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Db    113 TCGACTCCCGATCCAGATCTTCCCGGGAGCCGGGCCCTACCTGCCCTGCCCCGAGCGCCT  172

Qy     62 GCCTGCCCCAACAGCAGCAGGCGCCTGGTTCCCGGCCGGAGCCGAGCAGCAACGCA  121
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Db    173 GCCTGCCCCAACAGCAGCAGGCGCCTGGTTCCCGGCCGGAGCCGAGCAGCAACGCA  232

Qy    122 GCGCCGGCTCGGAGACGCGCAGCTGGACGCCGCCATCCCGCATCCCGGTCA  181
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Db    233 GCGCCGGCTCGGAGACGCGCAGCTGGACGCCGCCATCCCGCATCCCGGTCA  292

Qy    182 TCATCACGGCGGTCTACTCCGTAGTTGTTCGTCGTGGCTTGGTGGCTTGGTGGCAACTCGCTCGGTCA  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TCATCACGGCGGTCTACTCCGTAGTTGTTCGTCGTGGCTTGGTGGCTTGGTGGCAACTCGCTCGGTCA  352

Qy    242 TGTTCGTGATCATCCGATACACAAAGAAGACAGCAACCAACATTTACATATTTAACC  301
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Qy    302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA  361
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Qy    422 ACATGTTCACCAGCATCTTCACCTTGACTTCACCTGACACCCTGAAGGCAAAGATCATCAATATCT  481
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Db    533 ACATGTTCACCAGCATCTTCACCTTGACTTCACCTGACACCCTGAAGGCAAAGATCATCAATATCT  592

Qy    482 GCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT  541
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Db    593 GCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT  652

Qy    542 GCATCTGGCTGCGTCGTCATCTGGTCATCTCTGCAATAGTCCTTGGAGGCACCAAAG  601
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Db    653 GCATCTGGCTGCGTCGTCATCTGGTCATCTCTGCAATAGTCCTTGGAGGCACCAAAG  712

Qy    602 TCAGGGAAGAGTCGATGTCATTGAGTGCTCTCCTTGCAGTTCCCAGATGATGACTACTCCT  661
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Qy    662 GGTGGGACCTTCTGCTTGAAGATCGCGTCTTCATCTTTGCCTTGCCTTCGTCGTATCCCGTCCTCA  721
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Db    773 GGTGGGACCTTCTGCTTGAAGATCGCGTCTTCATCTTTGCCTTGCCTTCGTCGTATCCCGTCCTCA  832

Qy    722 TCATCATGTCTGCTGCTACACCCGGTCTCAAGAGCGTCGGTCTCAAGAGCGTCTCCTTCTG  781
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Qy    782 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCCTGGTGG  841
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Qy    842 CAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGACTCTGGGGA  901
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Qy    661 TGGTGGGACCTTCTGCTTGAAGATCGCGTCTTCATCTTTGCCTTGCCTTCGTCGTCCTC  720
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Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
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Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGAGGCTCTGGGG  900
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Qy    901 AGCACCTCCCACAGCACAGCACGTGCTCTCTCCAGCTATTACTTCTGCATTGCCTTAGGCTAT  960
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Db    901 AGCACCTCCCACAGCACAGCACGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTCACGCCTTTCTCTACGCCTTTCTCTTGAAAACTTCAAGCGGGTGT  1020
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Db    961 ACCAACAGTAGCCTGAATCCCATTCTCTCACGCCTTTCTCTACGCCTTTCTCTTGAAAAACTTCAAGCGGGTGT  1020

Qy   1021 TTCCGGGACTTCTGCTTCAGGATCTGCTTACCTGAGGACATCGATGGGATAATAAACCAGTA  1080
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Db   1021 TTCCGGGACTTCTGCTTCAGGATCTGCTTACCTGAGGACATCGATGGGATAATAAACCAGTA  1080

Qy   1081 CGAAATACAGTTCAGGATCTCAGGATCCTGCTTACCTGAGGGATGGGATGAATAAACCAGTA  1140
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RESULT 15
US-10-318-661-3
; Sequence 3, Application US/10318661
; Publication No. US2003016747A1
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP2
;   CURRENT APPLICATION NUMBER: US/10/318,661
;   CURRENT FILING DATE: 2003-05-05
;   PRIOR APPLICATION NUMBER: US 09/341,446
;   PRIOR FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 3
;   LENGTH: 1284
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified KOR
US-10-318-661-3

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Db   1253 G 1253
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Search completed: April 6, 2005, 13:18:07
Job time : 769.333 secs

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                         GenCore version 5.1.6
               Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         April 6, 2005, 12:28:42 ; Search time 4384.33 Seconds
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Title:          US-09-904-584-3
Perfect score:  1154
Sequence:       1 atggagctcccgatccagat..........ccagtatgactagtcgtgga 1154
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched:       3423544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	1	805.2	69.8	895	6	CB565888	CB565888 AGENCOURT
	2	581.8	50.4	762	7	CO960667	CO960667 AGENCOURT
c	3	518.8	45.0	784	7	CO960682	CO960682 AGENCOURT
	4	470.6	40.8	837	7	CF593603	CF593603 AGENCOURT
	5	466.4	40.4	480	5	BX092912	BX092912
	6	432.4	37.5	2405	3	AK038389	AK038389 Mus muscu
	7	421.6	36.5	4022	3	AK043873	AK043873 Mus muscu
	8	367.8	31.9	2919	3	AK038620	AK038620 Mus muscu
	9	367.8	31.9	2959	3	AK079529	AK079529 Mus muscu
	10	352	30.5	879	3	AY410745	AY410745 Homo sapi
	11	335.6	29.1	2940	3	AK044178	AK044178 Mus muscu
	12	327.4	28.4	2974	3	AK043275	AK043275 Mus muscu
	13	327	28.3	3101	3	AK031926	AK031926 Mus muscu
	14	325.8	28.2	879	9	AY410747	AY410747 Mus muscu
c	15	309.8	26.8	1053	9	CNS04C2T	CNS04C2T Tetraodon
	16	277.6	24.1	775	5	BX874804	BX874804
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	20	264.4	22.9	579	5	BP214141	BP214141
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	23	231.2	20.0	682	9	AY410746	AY410746 Pan trogl
	24	228	19.8	1176	9	AY400827	AY400827 Homo sapi
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	26	225	19.5	1176	9	AY400829	AY400829 Mus muscu
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ALIGNMENTS

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DEFINITION  AGENCOURT_12691503 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:6519213 5', mRNA sequence.
ACCESSION   CB565888
VERSION     CB565888.1  GI:29485418
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Guthrie cDNA Resource Center
            cDNA Library Preparation: Guthrie cDNA Resource Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBF001 row: f  column: 09
            High quality sequence stop: 763.
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                     /clone="IMAGE:6519213"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_146"
                     /tissue_type="mixed"
                     /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.presv.dat
                     a. Note: this is a NIH_MGC Library."
ORIGIN
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(Right column)

```
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 762)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Guthrie cDNA Resource Center
             cDNA Library Preparation: Guthrie cDNA Resource Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: IRBI8  row:d  column: 04
             High quality sequence start: 30
             High quality sequence stop: 549.
FEATURES             Location/Qualifiers
     source          1..762
                     /organism="Homo sapiens".
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7389810"
                     /tissue_type="mixed"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC 146"
                     /note="Vector: pcDNA3.1; Site_1: multiple; Site_2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.presV.dat
                     a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match        50.4%;  Score 581.8;  DB 7;  Length 762;
Best Local Similarity  97.1%;  Pred. No. 1.5e-141;
Matches 603;  Conservative  0;  Mismatches 17;  Indels 1;  Gaps 1;

Qy     1 ATGGACTCCCGATCCAGATCTTCGGCGGGAGCCGGGCCCTACCTGCGCCCGGCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    27 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGGCCCGAGCGCC 86

Qy    61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    87 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAGCAACGGC 146

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCTGGAGCCCGCGCCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCTGGAGCCCGCGCCACATCTCCCGGCCATCCCGGTC 206

Qy   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTGGTGGGCAACTCGCTGGTC 266

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   267 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 326

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTCACTTG 386

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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(Left column)

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Query Match        69.8%;  Score 805.2;  DB 6;  Length 895;
Best Local Similarity  97.1%;  Pred. No. 3e-200;
Matches 841;  Conservative  0;  Mismatches 23;  Indels 2;  Gaps 2;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGGCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGCCCGGCCCGAGCGCC 61

Qy    61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAGCAACGGC 121

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCCACATCTCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCCACATCTCCCGGCCATCCCGGTC 181

Qy   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGGCTGGTGGGCAACTCGCTGGTC 241

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 301

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 361

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 421

Qy   421 AACATGTTGACAGCCATCTCACCTTGACCATGATGAGGCTGACCGCTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 AACATGTTCACCAGCCATCTTCACCTTGACCATGATGAGGCTGACCGCTACATTGCCGTG 481

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCTTGAAGGCAAAGATCATCAATATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCTTGAAGGCAAAGATCATCAATATC 541

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 601

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC 661

Qy   661 TGGTGGGACTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCTGTCCTC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   662 TGGTGGGACTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 721

Qy   721 ATCATCATGTCTGCTACACCCTGATGATCCTGGTCTCAAGAGCGTC-GGCTCCTTTC 779
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   722 ATCATCATGTCTGCTACACCCTGATGATCCTGGTCTCAAGAGCGTCCGGGCTCCTTTC 781

Qy   780 TGGCTCCCGAGAGAAAGATC-GCAACCTGCGTAGGATCACCAGACTGGTTCTGGTGTGG 838
           ||||||||||||||||||| |||  ||||||||||||||||||||||||||||
Db   782 TGGCTCCCCAGAGAAAGATCNGCACCCTGCGTAGGATCACCAGACTGGTTCCCTGGTGTGG 841

Qy   839 TGGCAGTCTTCGTCGTCTGGACT 864
           || |||| ||||||| ||||||
Db   842 GTGGGCAGGTCTTCGTCCGTCTGGCT 867
```

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RESULT 2
CO960667

LOCUS       CO960667               762 bp    mRNA    linear    EST 17-AUG-2004
DEFINITION  AGENCOURT 30842630 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:7389810 5', mRNA sequence.
ACCESSION   CO960667
VERSION     CO960667.1  GI:51125223
KEYWORDS    EST.
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Db    387 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAGTTCCATTGATTACTAC 446

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 506

Qy    481 TGGCACCCCGTGAAGGCTTTGACTTCCGCCACACCCTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507 TGGCACCCCGTGAAGGCTTTGGACTTCCGCCACACCCTGAAGGCAAAGATCATCAATATC 566

Qy    541 TGCATCTGGCT-GCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGGACGCACCAA 599
          |||||||||||  ||||||||||||||||||||||||||| ||||||||||||||||||
Db    567 TGCATCTGGCTGCTGTCGTCATCTGTTAGCATCTCTGTTAGCATCCTTGGGGAGCGCAA 626

Qy    600 AGTCAGGGAAGAGACGTCGATGT 620
          ||  |||||||||||||||  ||
Db    627 AATCAGGGAAGAGACTCGAAGGT 647
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Query Match   45.0%; Score 518.8; DB 7; Length 784;
Best Local Similarity 97.6%; Pred. No. 5.3e-125;
Matches 537; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
Db    586 CTTGGAGGCACCAAAGTCAGGGAGGAGACGTCGATGCTCATTGAGTGCTCCTTGCAGTTCCCA 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 CCTTGAGGCACCAAAGTCA-GGAAGACGTCGATGCTCATTGAGTGCTCCTTGCAGTTCCCA 519

Qy    646 GATGATGACTACTCCTGGTGGGACCTCTTCATGAAGACTCGGTCTTCATCTTTGCCTTC 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 GATGATGACTACTCCTGGTGGGACCTCTTCATGAAGATCATCGGTCTTCATCTTTGCCTTC 459

Qy    706 GTGATCCTGTCCTCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGC 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GTGATCCCTGTCCTCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGC 399

Qy    766 GTCCGGCTCCTTTCTGGCTCCCGGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTG 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 GTCCGGCTCCTTTCTGGCTCCCGGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTG 339

Qy    826 GTCCTGGTGGTGGTGGIGGCAGTCTTCGTGCTGGACTCCCATCCCATTCACATATTCATCCTG 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 GTCCTGGTGGTGGTGGIGGCAGTCTTCGTGCTGGACTCCCATCCCATTCACATATTCATCCTG 279

Qy    886 GTGGAGGCTCTGGGGAGCACACCTCCCACAGCACAGCTGTCTCTCCAGTATTACTTCTGC 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278 GTGGAGGCTCTGGGGAGCACACCTCCCACAGCACAGCTGTCTCTCCAGTATTACTTCTGC 219

Qy    946 ATTGCCTTAGGCTATACCAAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 ATCGCCTTAGGCTATACCAAACAGTAGCCCGAAATCCCATTTTTACGCCTTTCTGGATGAA 159

Qy   1006 AACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAG 1065
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Db    158 GACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAG 99

Qy   1066 AGCACTAGCAGAGTCCGAAATACAGTTCAGATCCTGCTTACCTGAGGGGACATCGATGGG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 AGCACTAGCAGAGTCCGAAATACAGTTCAGATCCTGCTTACCTGAGGGGACATCGATGGG 39

Qy   1126 ATGAATAAAC 1135
          ||||  ||||
Db     38 ATGATGAACC 29
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FEATURES
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                     /clone="IMAGE:30531690"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     all-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."

ORIGIN

Query Match          40.8%;    Score 470.6;  DB 7;   Length 837;
Best Local Similarity 99.2%;    Pred. No. 2.5e-112;
Matches  473;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCGCCCGAGCGCC   60
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Db  240 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCGCCCGAGCGCC  299

Qy   61 TGCCTGCCCCCACAGCAGCGCCTGGTTTCCCGGCTGGGCCCGACAGCAACGGC  120
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Db  300 TGCCTGCCCCCACAGCAGCGCCTGGTTTCCCGGCTGGGCCCGACAGCAACGGC  359

Qy  121 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCCCGCCACATCTCCCCGGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  360 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCCCGCCACATCTCCCCGGTC  419

Qy  181 ATCATCACGGGCGGGTCTACTCCGTAGTGTTCGTCGTGGTGGCAACTCGCTGGTC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  420 ATCATCACGGGCGGGTCTACTCCGTAGTGTTCGTCGTGGTGGCAACTCGCTGGTC  479

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  480 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  539

Qy  301 CTGGCTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  540 CTGGCTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGAGTACGGTCTACTTG  599

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTCGTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 ATGAATTCCTGGCCTTTGGGGATGTCGTGTGCAAGATAGTAATTTCCATTGATTACTAC  659

Qy  421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCC  477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 AACATGTTCACCAGACATCTTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCC  716
```

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RESULT 5
BX092912
LOCUS         BX092912          480 bp    mRNA      linear     EST 23-JAN-2003
DEFINITION    BX092912 Soares placenta Nb2HP Homo sapiens cDNA clone
              IMAGp998B19190 ; IMAGE:134322, mRNA sequence.
ACCESSION     BX092912
VERSION       BX092912.1  GI:27823005
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 480)
AUTHORS       Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
              Radelof,U., Schneider,D. and Korn,B.
TITLE         Human UnigeneSet - RZPD3
```

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JOURNAL       Unpublished (2003)
COMMENT       Contact: Ina Rolfs
              RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
              Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
              RZPD; IMAGp998B19190.
              RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
              Human UnigeneSet - RZPD3 (RZPDLIB No.972)
              http://www.rzpd.de/CloneCards/cgi-
              bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
              RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
              Heubnerweg 6, D-14059 Berlin, Germany
              Tel: +49 30 32639 101
              Fax: +49 30 32639 111
              www.rzpd.de
              This clone is available royalty-free from RZPD;
              contact RZPD (clone@rzpd.de) for further information. Seq primer:
              M13r, Primer sequence: TTCACACAGGAAACAGCTATGAC.

FEATURES
     source          Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998B19190 ; IMAGE:134322"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares placenta Nb2HP"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5',
                     AACTGGAAGAATTCGGCGCCGCAGGAATTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo.  "

ORIGIN

Query Match          40.4%;    Score 466.4;  DB 5;   Length 480;
Best Local Similarity 99.8%;    Pred. No. 2.8e-111;
Matches  467;  Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy  687 CGTCTTCATCTTGCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCTACACCCTGAT  746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CGTCTTCATCTTGCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCTACACCCTGAT   60

Qy  747 GATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGTCCTCGTCGGTGGTGGTGGCGAAGAAGATCGCAACCT  806
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGTCCTCGTCGGTGGTGGTGGCGAAGAAGATCGCAACCT  120

Qy  807 GCGTAGGATCACCAGACTGGTCCTGGTGGTCCTGGTGGTGGTCGTCGTCGTCGTGGACTCC  866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCGTAGGATCACCAGACTGGTCCTGGTGGTCCTGGTGGTGGTCGTCGTCGTCGTGGACTCC  180

Qy  867 CATTCACATATTCATCCTGGTGGAGGCTCTGGGAGGCTCTGGGAGGCACCTCCCACAGCACAGCAGTCGTCT  926
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CATTCACATATTCATCCTGGTGGAGGCTCTGGGAGGCTCTGGGAGGCACCTCCCACAGCACAGCAGTCGTCT  240

Qy  927 CTCCAGCTATTACTTCTGCATTGCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCT  986
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCT  300

Qy  987 CTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAA  1046
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAA  360

Qy 1047 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA  1106
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA  420

Qy 1107 CCTGAGGGACATCGATGGATGAATAAACCAGTATGACTAGTCGTGGA  1154
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CCTGAGGGACATCGATGGATGAATAAACCAGTATGACTAGTCGTGGA  468
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RESULT 6
AK038389
LOCUS       AK038389              2405 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230002D02 product:opioid receptor, mu,
            full insert sequence.
ACCESSION   AK038389
VERSION     AK038389.1  GI:26332528
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2405)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,H., Konno,H., Kouda,M.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     LTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLR
                     RITRMVLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLNPV
                     LYAFLDENFKRCFREFCIPTSSTIEQQNSARIRQNTREHPSTANTVDRTNHQPTLAVS
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Matches  663;  Conservative   0;  Mismatches 336;  Indels  9;  Gaps   2;

Qy         92 CCGGCTGGGCCGAGCCCGACACAGCAACGGCAGCGCCGGCTCGGAGGACCGGCCAGCTGGAGC 151
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Db        159 CCGACCCATGCGGTCCTAACCCACGGGCGGCTTGGCGGGAGCCACAGCCTGTGCCCTCAGA 218

Qy        152 CCGCGCACATCTCCCCGGCCATCCGGTCATCATCACGGCGGTCTACTCCGTAGTGTTCG 211
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Db        219 CCAGCAGCCCTTCCATGTCACAGCCATCACCATCACCATGGCCCCTCTATTCTATCGTGTGTG 278

Qy        212 TCGTGGGCTTGGTGGGCAACTCCGTGGTCATGTTCGTGATCATCCGATACACAAAGATGA 271
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Db        279 TAGTGGGGCTCTTTGGAAACTTCCTGGTCATGTATGTGATTGTTAAGATATACCAAAATGA 338

Qy        272 AGACAGCAACCAACATTTACATATTTAACCTGGCTTTGCAGATGCTTTAGTTACTACAA 331
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Qy        332 CCATGCCCTTCCAGAGTACGGTCTACTTGAGTGATGAATTCCTGGGCTTTTGGGGATGTGCTGT 391
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Qy        392 GCAAGATAGTAATTCCATTGATTACTACAACATGTTCACCTTGACCA 451
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Db    579  CCCCCGAAATGCCAAAATGTCAATGTCTGCAACTGGATCCTCTTCTGCCATTGGTC  638
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Db    693  CCCTCACGTTCTCTCATCCCACATGGTACTGGGAGAACCTGCTC--AAAATCTGTGTCT  749

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Db    930  ACATCATGTCATCATCAAGGCACTGATCAAGCACTGCTTTCCAGAAACCCACTTTCCAGACTGTTT  989

Qy    932  GCTATTACTTCTGCATTGCATTGCCTTAGGCTATACCAACACAGTAGCCGATCCCATTCCTACG  991
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Db    990  CCTGGCACTTCTGCATTGCCTTGGGTTACACCAAAACAGCGTGCCTGGAACCCAGTTCTTTATG  1049

Qy    992  CCTTTCTTGATGAAAAACTTCAAGCGGTGTTCCGGGACTTCGCTTCTGCGGCTTTCCACTGAAGATGA  1051
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Db   1050  CGTTCCTGGATGAAAACTTCAAAACATGTTTTAGAGAGTTCTGCGATCCCGCCACTTCCTCCA  1109

Qy   1052  GGATGGAGCGGCAGAGCACTAGCAGAGTCCGAAATACAGTTCAGGATC  1099
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ACCESSION   AK043873
LOCUS       AK043873               4022 bp    mRNA           linear   HTC 03-APR-2004
DEFINITION  Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
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            RECEPTOR, full insert sequence.
ACCESSION   AK043873
VERSION     AK043873.1  GI:26335979
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10049636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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```
TITLE       RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
            Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4022)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp/,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
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            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK038620
VERSION     AK038620.1  GI:26332698
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED    11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2919)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
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Qy    273 GACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAAAC 332
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Qy    333 CATGCCCTTTCAGAGTACGGCTCTACTTGATGAATTCCTGGCCTTTGGGGATGTGCTGTG 392
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Db    405 GCTGCCCTTCCAGAGCCCTGTTGGCGCCGCCAAGTGCGGCGTCTGGG 464

Qy    393 CAAGATAGTAATTTCCATTGATTACTACAACATGTTCCACCAGCATCTTCACCTGACCAT 452
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Qy    633 CTTGCAGTTCCAGATGATGATGACTACTCCTGGTGGGACCTCTTCATGAAGAATCTGCGTCTT 692
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Db    705 GTTCCCCAGTCC------CAGCTGGTACTGGGACACTGTGACCAAGATCTGCGTGTT 755

Qy    693 CATCTTGCCTTCGTGATCCTCTGCTCTACACCCTGATGATCCT 752
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Db    756 CCTCTTTGCCTTCGTGTGTGCCGATCCTCATCATCACGGTGTGTCTATGGCCTCATGCTACT 815

Qy    753 GGCTGTCAAGAGCGTCCGGCTCCTTTCTGGCTCCCAGAGAAAGATCGCAACCTGCGTAG 812
          ||| ||||| | | ||||| |  ||  || ||  |  || ||||  | || | ||  ||
Db    816 GCGCCCTGCGCAGCGTGCGTGTCTGCTGTGCCGGTTCCAAGGAGGAGGACCGAGCCTGCGGCG 875

Qy    813 GATCACCAGACTGGTCTGGTTGTCCTGCGTCTTCGTGTCTGGACTCCCATTCA 872
          |||  |  | || |||||| | || |  | | || |||  ||| ||| |||| |
Db    876 CATCACGCGCAGTGTCGGTGGTGGGGGGCGCCTTCGTGTGTGGGGGCGCCCATCCA 935

Qy    873 CATATTCATCCTGGTGAGGGC---AGCACCTCCCACAGCACAGCTGCTCTCTC 929
          ||| ||||| || | |||||    || || |  ||  ||  |||||  || | |
Db    936 CATCTTCGTCATCGTCTGCGACCGCTGTGGACATCAATCGGCGCGACCCACTTGTGGTGGC 995

Qy    930 CAGGATTACTTCTGCATTGCCTTAGGCTCGTATACCAACAGCTAGCCTGAATCCATTCCTCTA 989
          |||  || || || || ||  |   | | || || |  | ||  |||||  ||||||||||||
Db    996 CGCAACTGCACCTGCATTGCGTCGGGCTTGGGCTCACACCGCCTCAACCCGGTTCCTCTA 1055

Qy    990 CGCCTTTTCTTGATGAAAACTTCAAGCCGGTGTTTCCGGGACTTCTG 1034
          || || | |  |  || | | ||||||| || ||| || ||| |||
Db   1056 CGCCTTCCTGACGACGAGAACTTCAAGCCGGTGCTTCTTCCGCCAGCTCTG 1100
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Qy    574  TCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGAGAGTCGATGTCATTGAGTGCTCC 633
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Db    718  CCTGTTGCCATCATGGGCTCAGCACAAGT------GGACGGATGAAGAGATCGAGTGCCTG 771

Qy    634  TTGCAGTTCCAGATGATGACTACTCCTGGTGGACACCTCTTCATGAAGATCTGGCTCTTC 693
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Db    772  GTGGAGATCCCGCCCCTCAGGA---CTATTGGGGCCCTGTATTTGCCATCTGCATCTTC 828

Qy    694  ATCTTTGCCTTCGTGATCCCTGTCCTCATCATCATCGTCTGCTACACCCTGATGATCCTG 753
           ||  |||  ||||||     |||||||||| ||| |||| ||||||||| |||||
Db    829  CTTTTTTTCCTTCATCATCACCCGGTTCTCTGATCATCTCTGTCTGCTACAGCCTCATGATTCGA 888

Qy    754  CGTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCGTAGG 813
           |||        ||||||| |||||  |||||||||| |||||||  || |||||||||||
Db    889  CGACTTCGTGGTGTGTCCGGCTTTCAGGCTCCCCAGGACCACCGGAACCTGCGACGC 948

Qy    814  ATCACCAGACTGGTCCTGGTGGTGGCAGTCTTCGTCCTGCTCGTGGACTCCCATTCAC 873
           ||||||||||||    |||| || ||||||  ||||||| |||||    |||||
Db    949  ATCACACGGCTGGTACTGGTAGTTGTGGCTCTGTTGTTGTGGGCGGTCTGGACACCGTGCAG 1008

Qy    874  ATATTCATCCTGGTGGAGGCTGTGGGAGCACCTCCACAGCACAGCTGTCTCTCCAGC 933
                  ||||  ||||||| ||||||||||  || |||||    |||||||||
Db   1009  GTCTTTGTCCTGGTTCAAGGACTGGGTGTTCAGCCAGGTGAGACTGCAGTAGCCATT 1068

Qy    934  TATTACTTCTGCATTGCCTTAGGCTATCACCAACAGTAGCCTGAATCCCATTCTCACGGC 993
                ||||| ||||  |||||| |||| ||||||    ||| |||| |||||||||
Db   1069  CTGGCGCTTCGACACGACCCTGGCATGTCAACAGTTGTCTCAATCCCATTCTCTATGCT 1128

Qy    994  TTTCTTGATGAAAAACTTCAAGCGGTTGTTCGGGGACTTCTGCTTTCCACTGAAGATGAGG 1053
               || ||||| ||||| ||||| | ||| |||||||| | |||||||||||||||
Db   1129  TTCTTGGATGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTGCGTGCTTCGCCCTGCAC 1188

Qy   1054  ATGGACGGCAGAGCACTAGCAGAGTCCGAAATCAGTTCAGGAT 1098
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Db   1189  CGGGAGATGCAGGTTTCTGATCGTGTGCGCCAGCATTGCCAAGGAT 1233
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RESULT 9
AK079529
LOCUS       AK079529               2959 bp    mRNA      linear    HTC 03-APR-2004
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230027D20 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK079529
VERSION     AK079529.1   GI:26348047
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,J., Nakamura,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
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COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
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                     SSKAQAVNVAIWALASVVGPVAIMGSAQVEDEEIECLVEIPAPQDYWGPVFAICIFL
                     FSFIPVLIISVCYSLMIRRLRGVRLLSGSREKDRNLRRITRLVLVVVAVFVGCWTPV
                     QVFVLVQGLVQPGSETAVAILRFCTAIGYVNSCLNPILYAFLDENFKACFRKFCCAS
                     ALHREMQVSDRVRSIAKDVGLGCKTSETVPRPA"
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                     /note="putative"
     polyA_site      2919
                     /note="putative"
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Query Match     31.9%;    Score 367.8;    DB 3;    Length 2919;
Best Local Similarity     63.4%;    Pred. No. 3.6e-85;
Matches   599;    Conservative    0;    Mismatches  337;    Indels    9;    Gaps    2;
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Qy    154  GCGCACATCTCCCGGCCATCCCGGTCATCATCACGGCGGCTCTACTCCGTAGTGTTCGTC 213
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Db    298  GCCTTCCTGCCCCTTTGGACTCAAGGTCACCATGTGCTGGGGGCTCTACTTGGCTGTGTGCATC 357

Qy    214  GTGGGCTTGGTGGGCAACTCGCTCGGCCTCGTCATGCCCGTGTCGTCATGTCATGCATGCA 273
              |||| ||| |||  |||||| |||     ||| |||| |||||| ||| ||||
Db    358  GGGGGGCTCCTGGGGAACTGCCTCGTCATGGTGGTCATCCTCAGGCACACCAAGATGAAG 417

Qy    274  ACAGCAACCAACATTACATATTAACCTGGCTTTGGCAGATGCTTTAGTACTACAACC 333
           ||| ||||||||||||||||   ||  ||||| |||||| ||||| |||| ||||||
Db    418  ACTGCTACCAACATTTACATATTTAATCTGGCACTGGCTGATACCCTGGTCTTGCTGACA 477

Qy    334  ATGCCCCTTCAGATACGGTCCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGTGC 393
           ||| |||||  ||  ||| ||||||  |||||    |||||||| |||| |||  ||||
Db    478  CTGCCCTTCCAGGGCACAGACATCCTTCTGGGCTTTTGGCCATTTGGGAATGCACTGTGC 537

Qy    394  AAGATAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATG 453
           |||| |||   |||  ||  |||||||| |||||    ||||| ||||||||||||
Db    538  AAGACGGTCATTGCTATCGACTACTACAACATGTTTACCAGCACTTTCACTTTGACTGCC 597

Qy    454  ATGAGGTGGACGACCGGTCTACCTGTGCCACCCGTGAGGCTTTGGACTTCCCACA 513
           ||||| ||||| |||| ||||    || ||| ||||| |  |||||||||| |||
Db    598  ATGAGTGTAGACCGTTATGTAGCTATCTGCCACCCTATCCGTGCCCTTGATGTTCGGACA 657

Qy    514  CCCTTGAAGGCAAAGATCATCAATATCTGACCATCTGGCCGTGTCATCTGTTGGCATC 573
           |||  ||||| ||||  |||||  |   |||||   |||  |||| || |||| ||||
Db    658  TCCAGTAAAGCCCAGGCCGTTAATGTGGCCATATGGGCCCTGGCTTCGGTTGTGGTTGGT 717
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JOURNAL     sequencing pipeline with 384 multicapillary sequencer
            Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2959)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K. Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            Tel:81-45-503-9222, URL:http://genome.gsc.riken.jp/,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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Query Match          31.9%;  Score 367.8;  DB 3;  Length 2959;
Best Local Similarity  63.4%;  Pred. No. 3.6e-85;
Matches 599;  Conservative 0;  Mismatches 337;  Indels 9;  Gaps 2;

Qy    154  GCGCACATCTCCCCGGCCATCCGGTCATCATCACGGCGGCGGTCACTCCGTAGTGTTCGTC  213
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Db    341  GCCTTCCTGCCCCTTGGACTCACAAGGTCACCATCCGTGGGGCTCACTTGCCGTCGTGTGCATC  400

Qy    214  GTGGGCTTGGTGGGCAACTCGCTCTGTCGTGTCATGTTCGTGATCATCGGCGACATACAAAGATGAAG  273
           |  |||  ||| ||| ||||  |||| || || |||| || |||  ||  |||  ||  || |||||||
Db    401  GGGGGGCTTCCTGGGGAACTGCCTCGCCTCGTCATGTATGTCATCCTCAGGCACACCAAGATGAAG  460

Qy    274  ACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAACC  333
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Qy    334  ATGGCCCTTTCAGATGACGGTCTACTTGGATGAATTCCTGGCCCTTTGGGATGGTGCTGTGG  393
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Db    521  CTGCCCTTTCAGGGCACAGACATCCTTCTGGGCTTCTGGTTCCATTTGGAATGCACTGTGC  580

Qy    394  AAGATAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATG  453
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Db    581  AAGACGGTCATTGCTATCGACTACAACATGTTTACCAGCACTTTCACTTTGACTGCC  640

Qy    454  ATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCGTGAAGGCTTTGGACTTCCGCACA  513
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Db    641  ATGAGTGTAGACCGTTATGTAGCTATCTGCCACCCTATCCGTGCCCTTGATGTTCGGACA  700

Qy    514  CCCTTGAAGGCGAAAGATCATCAATATCTGCATCTGGCTGGTCATCTGTTGGCATC  573
           ||    ||  || |||  ||||  || | | || |||| | |  || | || ||
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Qy    574  TCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGACGTCGATGTCATTGAGTGCTCC  633
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Qy    634  TTGCAGTTCCAGATGACTGACTACCTGGTGGGGGACCTTCCTCATGAGAATCTGCGTCTTC  693
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Qy    694  ATCTTTGCCTTCTCGATCCGTCCTCATCATCGTCTGCTGCTACACCCCTGATGATCCTG  753
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Db    872  CTTTTTTCCTTCATCATCCCGGTTCTGATCATCTCTGTCTGCTACAGCCTGATGATTCGA  931

Qy    754  CGTCTCAAGAGCGTCGGCGTCCTCTTCTCGGCTCCTTGGACGTGCAACCTGGTAGG  813
           |  || |||  |||| | ||  ||    || ||  | || | | |||  ||| |
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Qy    814  ATCACCAGACTGGTCCTGGTGGTGGTGGCAGTCTTCGTCGGCTGCTGGACTCCCATTCAC  873
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Qy    874  ATATTCATCCTGGTGGAGGGCTCGGGGAGCGGCTCGGGAGACTGCTCCTCTCCCAGC  933
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Qy    934  TATTACTTCTGCATTGCTTAGGCTATACCAACAGTAGCCTGAATCCATTCTCTACGCC  993
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Qy    994  TTTCTTGATGAAAACTTCAAGGCGTGTTTCCGGGACTTCTGCTGCTTCCACTGAAGATGAG  1053
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Db    1172 TTCTTGGATGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTGCTGTGCCTCTGCCCTGCAC  1231

Qy    1054 ATGGAGCGGCAGAGCACTAGCAGAGTCCGAAATACAGTTCAGGAT  1098
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Db    1232 CGGGAGATGCAGGTTTCTGATCGTGTGCGCAGCATTGCCAAGGAT  1276
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RESULT 10
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LOCUS   AY410745   879 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Homo sapiens OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY410745
VERSION   AY410745.1 GI:39766713
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
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Qy   260 ACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTT 319
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Db   2 ACACCAAAATGAAGACAGCCCAATATTTACATCTTTAACCTGGCCCCTGGCCGACACTC 61

Qy   320 TAGTTACTACAACCATGCCCTTTCAGAGTACGGTACGGTCTACTTGATGAATTCCTGGCCTTTTG 379
              | || |||| || ||||| ||||| | ||||| | ||| ||| || | ||||| ||||
Db   62 TGGTCCTGCTGACGCGTGCCCCTTCCAGGGCACGGCACATCCTCTGGGCTTCGGCCCGTTTG 121

Qy   380 GGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCT 439
              || ||| |||||||||||| ||| |||| |||| |||||||||||||||||||||||| ||
Db   122 GGAATGCGCGTGTGCAAGACAGTCATTGCCATTGACTACTACAACATGTTCACCAGCACCT 181

Qy   440 TCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTT 499
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Db   182 TCACCCTAACTGCCATGAGTGTGGATCGCATCGTGAGCCTATCGCCATCCGTGCCC 241

Qy   500 TGGACTTCCGCACACCCTTGAAGGCAAAGATCATCATAATATCTGCATCTGGCTGCTGTCGT 559
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Qy   560 CATCTGTTGGCATCCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAGACGTCGATG 619
              | ||| |||| |||| || |||| | ||| || |||| | || |||||| |
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Qy   620 TCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCTGGTGGGACCTTCATGA 679
              | | | || ||| |||||| ||||| || | || || || || |||||| || ||
Db   356 AGATACGAGTGCCTGGTGGAGATCCTGCAGGATTAC---TGGGGGCCCGGTGTTTG 412

Qy   680 AGATCTGGCGTTCATCTTTGCCTTCGTGATCCTCATCATCATCATCGTCTGCTACA 739
              ||| |||| ||| |||| || |||| |||||||||||||||||| || ||||||
Db   413 CCATCTGCATCTTCCTCTTCCTTCATCGTCCATCGTCGTCATCTCTGTCTGCTACA 472

Qy   740 CCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATC 799
              || |||||||| ||| | || || || ||| |||| || || |||||||||| || ||
Db   473 GCCTCATGATCCGGCGGCTTCGGTGGAGTCCGCCTCCTGGCTCCCGAGAGGAGGGACC 532

Qy   800 GCAACCTGGCTAGGAGATCACCAGACTGGTCTGGTGTCCTCGTGGTGTGGCAGTCTTCGTCGTCTGCT 859
              | |||||| | | ||||||| | ||||| |||| | || || || ||| | |||| ||| ||
Db   533 GGAACCTGCGGGCGGCCATCACCTCGGCTGGTGGTGCTGGTGGTAGTGGCTGTGTCGTGGGCTGCT 592

Qy   860 GGACTCCCATTCACATATTCATCCGGTGAGGCTGCTGCGAGGGCTCTGGGAGGCACCCCACAGCACAG 919
              |||| ||| | || | ||| || ||| ||| ||| ||| || || || |||| | || |||| |||
Db   593 GGACGCCGTGTCCAGGTCTTCGTGCGTGCTGGCCCAAGGGCTGGGGGGGTTCAGCCAGCCGAGA 652

Qy   920 CTGCTCCTCCCAGCTATTACTTCTGCATTGCCTTAGGCTATACCAACAGTAGCCTGAATC 979
              |||| | |||| | || || |||| | || | || ||| || |||||| |||| |||
Db   653 CTGCCGTGGCCATTCTGCGGCTTCTGCACCGCGCCCGGCCTACGTCAACAGCTGCCTCAACC 712

Qy   980 CCAATTCTCTACGCCTTCTTGATGATGAAAACTTCAAGCGGTGTTTCCGGGGACTTCGTCGTTTC 1039
              ||||| |||| ||||||||| ||||| || ||||||| | ||| | ||| | ||| ||| ||
Db   713 CCATCCTCACGCCTTCTCCTGATGAGAACTTCAAGGCCTGTCTTCCGCAAGTTCTGTGTG 772

Qy   1040 CACTGAAGATGAGGATGGAGCGGGACGTGCAGAGGCACTAGCAGAGTCCGAAATACAGTTCAGGA 1097
              ||||| ||| || |||| |||||||||| | | | | |||| | | | | | || |||| |
Db   773 CATCTGCCCTGCGCCGGGACGTGCTGCAGGTGCTGACCCGCCGTGGCGCAGCCATTGCCAAGGA 830

RESULT 11
AK044178
LOCUS   AK044178   2940 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830097K10 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK044178
VERSION   AK044178.1 GI:26090219
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   99279253
  MEDLINE   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,M., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection

```
Qy   315  TGCTTTAGTACTACAACCATGCCCTTTCAGAGTACGGCTCACTTGATGAATTCCTGGCC  374
          |||||| ||||||  |||||||  |||| ||| |||||||||||||||||||| ||||||
Db   483  TACCCTGGTCTTGCTGACACTGCCCTTCCAGGGCACAGACATCCTTCGGGCTTCTGGCC  542

Qy   375  TTTTTGGGATGTGCTGTGCAAGATAGTAATTCCTTGATTACTACAACATGTTCACCAG  434
          ||||| |||||||||||||||||| |||||   ||| |||||||||||||||| |||||
Db   543  ATTTGGGAATGCACTGTCAAGAGACGGTCATTGCTATCGACTACTACAACATGTTTACCAG  602

Qy   435  CATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCGTGCACCCCGTGAA  494
          ||    ||||||||||    |||    ||||||  || ||||||||||||||||||
Db   603  CACTTCACTTTGACTGCCATGAGCGTTATGTGACCGTTATGTAGCTATCTGCCACCTATCCG  662

Qy   495  GGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCT  554
          |||||||||   |||| ||||| ||||| |||| || ||||||| |||| ||||||||||
Db   663  TGCCCCTGATGTTCGGACATCCAGTAAAGCCCAGGCCCGTTAATGTGGCCATATGGGCCCT  722

Qy   555  GTCGTCATCTGGTTGGTGTTCCTGTTGCCATCATGGGCTCAGCACAGT-----GGAGGA  776
          |||||||    |||| ||||  |||||||||| ||||||||||||||        |||||
Db   723  GGCTTTCGGTGGTTGGTGTTGTGTTCCTGGTGTGGGGACCTTGGGGACCTCTT  674

Qy   615  CGATGTCATTGAGTGCTCCTCGCAGTTCCCAGATGATGACTACTCCTGGTGGGACCTCTT  674
          ||  ||||||  ||||  |||||||||    ||     ||||| ||||||  |||||  |
Db   777  TGAAGAGATCGAGTGCCTCGTGGAGGATCCCGCCCTCCGGA---CTATTGGGGCGCCCTGT  833

Qy   675  CATGAAGATCTGCTTCATCTTTGCTTCGTGTCCTCATCCCGTCCTCATCATCGTCTG  734
          || |||||||| || ||||  |||||| |||| ||||||| | |||||||||||||||
Db   834  ATTTGCCATCGCATCTTCCTTTTTCCTTCATCATCCCGTTCGATCATCTCTGTCTG  893

Qy   735  CTACACCCTGATGATCCTGCGTCCAAGAGCGGTCCGGCCCTTTCTGGCTCCCCGAGAGAA  794
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Db   894  CTACAGCCTCATGATTCGACGACTTCGTGTGTCCGGCTCCTTTCAGGCTCCCCAGAGAGA  953

Qy   795  AGATCGCAACCTGCGTAGGATCACCAGACTGCGTCCTGGTGGTGGGCAGTCTTCGTCGT  854
          ||  || |||||  ||||  |||| ||||  |||||| ||||| ||  ||||||||| |
Db   954  GGACCGGACCTGCGCACGCATCACACGCGGTACTGGTGGTAGTTGTGTGTTTGTTGTGGG  1013

Qy   855  CTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGAGCACCTCCCACAG  914
          |||||||||  ||||||||||| ||||||||| ||| || ||||||||| || |||||||
Db  1014  CTGCTGGACACCTGTCAGGTCTTGTTCCTGGTTCAAGGACTGGGTGTTCAGCCAGGTAG  1073

Qy   915  CACAGCTGCTCTCTCCAGCTATTACTTCTGCAATGCCTTAGGCATACCAACAGTAGCCT  974
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Db  1074  TGAGACTGCAGTAGCCATTCTGCACAGCCCTGGGCATGTCAACAGTTGTCT  1133

Qy   975  GAATCCCATTCTCTACGGCCTTTCTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTG  1034
          |||||||||| |||  ||||| ||||| ||| ||||||| |||  |||||||||||| ||
Db  1134  CAATCCCATTCCTATGCTTCTTGGATGAGAACTTCAAGGCCTGTTTAGAAGTTCTG  1193

Qy  1035  CTTTCCACTGAACATGAGGATGCGGCAGAGCACTAGCAGAGTCCGAAATACAGTTCA  1094
          ||||||||||| ||||| |||| ||||||||||||| ||| |||||| |||| |||||
Db  1194  CTGTGCTTCTGCCCGCACCGGGAGATGCAGCGGTTTCTGATCGTGTCGGCGCAGCATTGCCAA  1253

Qy  1095  GGAT  1098
          ||||
Db  1254  GGAT  1257
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RESULT 12

AK043275

LOCUS   AK043275   2974 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION   Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
               enriched library, clone:A730079L19 product:NOCICEPTIN RECEPTOR
               (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK043275
VERSION   AK043275.1 GI:26089596
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.

JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2940)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
               Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
               Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
               Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
               Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
               Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
               Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
               Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
               Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
               Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
               Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
               Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
               Physical and Chemical Research (RIKEN), Laboratory for Genome
               Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
               RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
               Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp/,
               URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
               Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
               Encyclopedia Project of Genome Exploration Research Group in Riken
               Genomic Sciences Center and Genome Science Laboratory in RIKEN.
               Division of Experimental Animal Research in Riken contributed to
               prepare mouse tissues.
               Please visit our web site for further details.
               URL:http://genome.gsc.riken.jp/
               URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
     source   1..2940
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="C57BL/6J"
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                   /clone="A830097K10"
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                   (SWISSPROT|P35377, evidence: FASTY, 97.1%ID, 100%length,
                   match=1135)"
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                   /note="putative"
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                   /note="putative"
ORIGIN

Query Match   29.1%; Score 335.6; DB 3; Length 2940;
Best Local Similarity   61.9%; Pred. No. 1e-76;
Matches 597; Conservative 0; Mismatches 339; Indels 28; Gaps 3;

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Qy   154  GCGCACATCTCCCCGCCCATCCGGTCATCATCACGGCGGTCACTTAGTTCGTC
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Db   303  GCCTTCCTGCCCCTTGGACTCAAGGTCACCATCGTGGGGCTCACTTGGCTGTGTGCATC  362

Qy   214  GTGGGCTTGGTGGGCAACTCGCTCGGTCATGTTCGTGATCAT-------------  254
          | |||| |||||| ||   ||  ||||| |||| |||   |||
Db   363  GGGGGGCTCCTGGGAACTGCCTCGTCGTCATCTGGGAGGGCATTGAGGGGAACTGGAGACAG  422

Qy   255  CCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCCAGA  314
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  TITLE       High-efficiency full-length cDNA cloning
  JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE     99279253
  PUBMED      10349636
REFERENCE   2
  AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
              Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
              prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE     20499374
  PUBMED      11042159
REFERENCE   3
  AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
              Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
              Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
              Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
              Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
              Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
              Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE       RIKEN integrated sequence analysis (RISA) system-384-format
              sequencing pipeline with 384 multicapillary sequencer
  JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE     20530913
  PUBMED      11076861
REFERENCE   4
  AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
              FANTOM Consortium.
  TITLE       Functional annotation of a full-length mouse cDNA collection
  JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
              Group Phase I & II Team.
  TITLE       Analysis of the mouse transcriptome based on functional annotation
              of 60,770 full-length cDNAs
  JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2974)
  AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
              Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
              Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
              Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
              Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
              Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
              Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
              Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
              Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
              Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
              Takeda,Y., Tanaka,A., Tomaru,A., Toya,T., Yasunishi,A.,
              Muramatsu,M. and Hayashizaki,Y.
  TITLE       Direct Submission
  JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
              Physical and Chemical Research (RIKEN), Laboratory for Genome
              Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
              RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
              Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
              URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
              Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /clone="A730079L19"
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="7 days neonate"
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     polyA_site      2974
                     /note="putative"
ORIGIN

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Best Local Similarity 63.4%;   Pred. No. 1.5e-74;
Matches  537;  Conservative    0;  Mismatches  301;  Indels   9;  Gaps    2;

Qy        252 CATCCGATACACAAAGATGAAGACAGCAACCACATTACATATTTAACCTGGCTTTGGC 311
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Db        450 CAGCAGGCACCACCAAGATGAAGAGACTGCTACCAACATTTACATATTTAATCTGGCACTGGC 509

Qy        312 AGATGTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTG 371
              ||||||||| ||||||||||||||||| |||||||||||||  |||  ||||| |||  |||
Db        510 TGATACCCTGGTCTTGCTGACACTGCCCCTTCCAGGGCACAGACATCCTTCTGGGCTTCTG 569

Qy        372 GCCTTTGGGGATGTCGTGTGCAAGATAGTAATTCCATTGATTACTACAACATATGTCAC 431
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Db        570 GCCATTTGGGAATGCACTGTTGCAAGACGGTCATTGCTATCGACTACTACAACATGTTTAC 629

Qy        432 CAGCATCTTCACCTTGACCATGATGAGCGTGGACGTGAAGAGGCTCAGCACAGCTCCACCCGT 491
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Db        630 CAGCACTTCACTTTGACTGCCATGAGTGTAGACCGTTATGTAGCTATCTGCCACCCTAT 689

Qy        492 GAAGGCTTTGGACTTCCGACACACCCTTGAAGCGCAAAGATCATCAATATCTGCATCTGGCT 551
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Db        690 CCGTGCCCTTGATGTTCGGACATCCAGTCAGTAAAGCCCAGGCCGTTAATGTGGCCATATGGGC 749

Qy        552 GCTGCTGCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGA 611
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Db        750 CCTGGCTTCGGTGGTTGGTGTTCCTGTTGCCATCATGGGCTCAGCACAAGT-----GGA 803

Qy        612 CGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCCTGGTGGGACCT 671
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Db        804 GGATGAAGAGATCGAGTGCGTCCGGTGGTGAGATCCCCAGGA---CTATTGGGGGCCC 860

Qy        672 CTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTGATCCCTGTCCTCATCATCATCGT 731
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Db        861 TGTATTTGCCATCTGCATCTTCCTTTTTCCTTCATCATCCCGGTTCGATCATCTCTGT 920

Qy        732 CTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCGCTCCTTTCTGGCTCCCGAGA 791
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Db        921 CTGCTACAGCCTCATGATTCGACGACTTCGTGGTGTGT|CCGGCTGCTTTCAGGCTCCCGAGA 980

Qy        792 GAAAGATCGCAACCTGCGTAGGATCACCAGAGATCACAGACGGCTGGCTGGCAGTCTTCGT 851
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Db        981 GAAGGACCGGAACCTGCGACCGCATCACACGGCGTACTGGTAGTGTGGTGTGTGTTTGT 1040

Qy        852 CGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGAGCACCTCCA 911
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Db       1041 GGGCTGCTGGACACCTGCAGGTCTTTGTCCGGTTCAAGGACTGGGTGTTCAGCCAGG 1100

Qy        912 CAGCAGCTGCTGCTCTCCAGCTATTACTTCGCAATGCCTGAGAAAACTTCAAGCGGTGTTCT 971
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Qy        972 CCTGAATCCCATTCTTCCTTCTTGATGAAAATCCGCAATCCCGGTTTCGGGAGAGCATTGC 1031
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Db       1161 TCTCAATCCCATTCTCATGCTTCTTGGATGAGAACTTCAAGGCCCTGCTTTAGAAAGTT 1220

Qy       1032 CTGCTTTCCACTGAAGATGAGAGATGGAGCGGCAGAGCACTAGCAGAGTCCGAAATACAGT 1091
              ||||||| ||||| |||||||||||| ||||||| |||||||||||||||||||||||||
Db       1221 CTGCTGTGCTTCTGCCCTGCACCGGGAGATGCAGGTTTCTGATCGTGTCGCCAGCATTGC 1280
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Qy    1092 TCAGGAT 1098
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Db    1281 CAAGGAT 1287
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RESULT 13
AK031926
LOCUS   AK031926   3101 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
            enriched library, clone:6330500C19 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK031926
VERSION   AK031926.1 GI:26082601
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
  PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3101)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
```

COMMENT     Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
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                     /db_xref="taxon:10090"
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Qy    494 AGGCTTTGGACTTCCGCACACCTTGAAGGCAAAGATCATCAATAATCGCATCGGCTGC 553
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RESULT 14

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DEFINITION Mus musculus OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY410747
VERSION   AY410747.1 GI:39766715
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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COMMENT   This sequence was made by sequencing genomic exons and ordering
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LOCUS   CNS04C2T   1053 bp   DNA   linear   GSS 01-SEP-2000
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ACCESSION   AL283934
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            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1

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AUTHORS     Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE       Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL     Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE     20296633
PUBMED      10835645
REFERENCE   2
AUTHORS     Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Genome Res. 10 (7), 939-949 (2000)
MEDLINE     20359837
PUBMED      10899143
REFERENCE   3  (bases 1 to 1053)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
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Matches 587;  Conservative 8;  Mismatches 230;  Indels 74;  Gaps 7;

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Qy    317 CTTTAGTTACTACAACAGTGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTT 376
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Qy    554 TGTGTCGTCATCTGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAGTCAGGGAGACG 613
Db    681 TCTCCCTCAGCCGTCGGAGTCCCCGTGATGATGGCAGCGACGACGAAGGAGACGATAAAG 622

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Qy    618 -------TGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCTGGTTGGAC 669
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Qy    790 GAGAAAGATCGCAACCTGCGTAGGATCACCAGGACTGGTCCTGGTGGTGGCAGTCTTC 849
Db    385 GAGAGGACGAGGAACCTCCGGCGGATCACCCGGCATGGTCCTGGTGGTGGTGGCGGCCTTC 326

Qy    850 GTCGTCTGTGGACTCCCATTCACATATTCATCCTGGTGGAGGTCTCGGGAGCACCTCC 909
Db    325 ATCGTCTGCTGRACTCCCATCCACATCTTCATCATCGTCAGGACGGTGGTGTCCATCGAC 266

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Qy    967 AGTAGCCTGGAATCCCATTCTCACGCCTTTCTCGATGAAAACTTCAAGCCGGTGTTTCCGG 1026
Db    205 AGCAGCCTGAACCCGGTCCTTCACGCCTTTCCTGGAGGAGAACTTCAAAAGGTGCTTCAGG 146

Qy   1027 GACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTCCGAAA 1085
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OM nucleic - nucleic search, using sw model

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Searched:     4708233 seqs, 2422607955 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result          %      Query
No.    Score  Match  Length  DB   ID          Description
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  1   1152.4  99.9    1154    9   HSU17298    U17298 Human kappa
  2   1152.4  99.9    1179    6   CQ723157    CQ723157 Sequence
  3   1152.4  99.2    1604    9   HUMOPRK1B   L37362 Homo sapien
  4   1144.4  99.2    1182    6   AR270854    AR270854 Sequence
  5   1144.4  99.2    1182    6   AX548862    AX548862 Sequence
  6   1144.4  99.2    1182    6   AX774764    AX774764 Sequence
  7   1144.4  99.2    1182    9   HSU11053    U11053 Human kappa
  8   1141.4  98.9    1182    9   AR281679    AR281679 Sequence
  9   1140.4  98.8    1142    6   A48343      A48343 Sequence 1
 10   1140.4  98.8    1142    6   AR141371    AR141371 Sequence
 11   1138.2  98.6    1143    6   AF498922    AF498922 Homo sapi
 12   1136.2  98.5    1143    6   AR281680    AR281680 Sequence
 13   1130.2  97.9    1143    6   AX280919    AX280919 Sequence
 14   1056.8  91.6    1396    9   AY168006    AY168006 Homo sapi
 15    999.4  86.6    1275    6   AR281681    AR281681 Sequence
 16    994.6  86.2    1275    6   AR281682    AR281682 Sequence
 17    930.6  80.6    1733   10   CPU04092    U04092 Cavia porce
 18    912.4  79.1    1273   10   RATRORD     D16534 Rattus norv
 19    912.4  79.1    1358   10   RATKOR1A    L22001 Rat kappa o
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 20   910.8  78.9    4742   10   RNU00442       U00442 Rattus norv
 21   909.2  78.8    1288   10   S81111         S81111 kappa-opioi
 22   909.2  78.8    1408    6   A68828         A68828 Sequence 5
 23   909.2  78.8    1408    6   AR409589       AR409589 Sequence
 24   909.2  78.8    1410    6   AR105149       AR105149 Sequence
 25   909.2  78.8    1410    6   AR178399       AR178399 Sequence
 26   909.2  78.8    1410   10   MUSKAPOPRE     L11065 Mouse kappa
 27   909.2  78.8    2094    6   RATKOR1B       L22536 Rattus norv
 28   909.2  78.8    2481    6   E08874         E08874 cDNA coding
 29   909.2  78.8    2481   10   RATKOR         D16829 Rattus norv
 30   869.6  75.4    1000    6   AR105156       AR105156 Sequence
 31   869.6  75.4    1000    6   AR178406       AR178406 Sequence
 32   632.2  54.8     757    4   PIGKOR         L49437 Sus scrofa
 33   590.2  51.1     715    4   AF012105       AF012105 Sus scrof
 34      577  50.0    1941    5   AY725197       AY725197 Taricha g
 35   544.4  47.2  179356    2 c AC083844       AC083844 Homo sapi
 36   544.4  47.2  183519    5 c AC009646       AC009646 Homo sapi
 37   512.2  44.4    1454    5   AF530573       AF530573 Rana pipi
 38   486.6  42.2    1477    5   AF285173       AF285173 Danio rer
 39   469.2  40.7     562   11   BV209418       BV209418 Danio rer
 40   453.6  39.3    1120    5   AY728087       AY728087 OPRK1_334
 41   449.4  38.9    1387    5   AF132813       AF132813 Taricha g
 42   446.4  38.7    2135    5   AR148257       AR148257 Danio rer
 43   446.4  38.7    2135   10   RATMUOR1A      L20684 Sequence
 44   446.4  38.7    2397   10   RATRORB        D16349 Rattus norv
 45   444.8  38.5    1401   10   RATMOPIOID     L22455 Rat mu opio
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ALIGNMENTS

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LOCUS       HSU17298                1154 bp    mRNA    linear   PRI 14-JUL-1995
DEFINITION  Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION   U17298
VERSION     U17298.1  GI:596069
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1154)
  AUTHORS   Simonin,F., Gaveriaux-Ruff,C., Befort,K., Charron,G., Bloch,B. and Kieffer,B.
  TITLE     kappa-Opioid receptor in humans: cDNA and genomic cloning,
            chromosomal assignment, functional expression, pharmacology, and
            expression pattern in the central nervous system
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)
  MEDLINE   95350200
  PUBMED    7624359
REFERENCE   2  (bases 1 to 1154)
  AUTHORS   Mansson,E., Bare,L. and Yang,D.
  TITLE     Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL   Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE   94338360
  PUBMED    8060324
REFERENCE   3  (bases 1 to 1154)
  AUTHORS   Kieffer,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Superieure De
            Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Illkirch,
            67400, France
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
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CDS              1..1143
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                 /protein_id="AAC50158.1"
                 /db_xref="GI:596070"
                 /translation="MDSPIQIFRGEPGPTCAPSACLPPNSAWFPGWAEPDSNGSAGS
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                 CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                 YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                 LVVVAFVVCWTPIHIFILVEALGSTHSTAALSSYYFCIALGYTNSSLNPILYAFLD
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ORIGIN

Query Match       99.9%;  Score 1152.4; DB 9; Length 1154;
Best Local Similarity  99.9%;  Pred. No. 3e-202;
Matches 1153; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC  60
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Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC  60

Qy     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC  120
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Db     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCGGAGCCCGACAGCAACGGC  120

Qy    121 AGGCGCGGCTCGGAGGACGGCGCAGCTGGACTCCCGGCAGCCCGGCCCGCCACATCTCCCCGGCCATCCCGGTC  180
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Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
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Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
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Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
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Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCGTCAAGATAGTAATTTCCATTGATTACTAC  420
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Db    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCGTCAAGATAGTAATTTCCATTGATTACTAC  420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
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Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
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Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTGGAGTAGTCCTTGGAGGCACCAAA  600
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Db    541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTGGAGTAGTCCTTGGAGGCACCAAA  600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
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Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTTGTCATCCCTGTCCTC  720
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Db    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTTGTCATCCCTGTCCTC  720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGAGACTCAAGAGCGTCCGGCTCCTCTCT  780
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Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGAGACTCAAGAGCGTCCGGCTCCTCTCT  780

Qy    781 GGCTCCCGAGAAAGATCCGAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
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Db    781 GGCTCCCGAGAAAGATCCGAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840

Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGAGGCTCTGGGG  900
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Db    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGTGGAGGCTCTGGGG  900

Qy    901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
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Db    901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTACGCCTTTCTTGATGAAATTTCAAGCGGTGT  1020
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Qy   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
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Db   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
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Db   1141 TGACTAGTCGTGGA  1154
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RESULT 2
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CQ723157
LOCUS       CQ723157                 1179 bp    DNA        linear       PAT    03-FEB-2004
DEFINITION  Sequence 9091 from Patent WO02068579.
ACCESSION   CQ723157
VERSION     CQ723157.1  GI:42284014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1179)
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 9091 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1..1179
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

Query Match       99.9%;  Score 1152.4;  DB 6; Length 1179;
Best Local Similarity  99.9%;  Pred. No. 3e-202;
Matches 1153; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCGCGCGGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC  60
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Qy    121 AGGCGCCGGCTCGGAGGACGCGGCAGTCGGACTCCCGGCACATCTCCCCGGCCATCCCGGTC  180
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Db    131 AGGCGCCGGCTCGGAGGACGCGGCAGTCGGACTCCCGGCACATCTCCCCGGCCACATCCCGGTC  190

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
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Db    191 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  250
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1604)
AUTHORS   Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and
              Liu-Chen,L.-Y.
TITLE   Cloning of a human .kappa. opioid receptor from the brain
JOURNAL   Life Sci. 56, 201-207 (1995)
COMMENT   Original source text: Homo sapiens (clone d2-115) (tissue library:
              genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA
              to mRNA.

FEATURES   Location/Qualifiers
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                     /dev_stage="fetus"
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     gene   1..1604
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                     /db_xref="GDB:G00-132-651"
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                     LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
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ORIGIN
Query Match   99.9%;   Score 1152.4;   DB 9;   Length 1604;
Best Local Similarity 99.9%;   Pred. No. 3e-202;   .
Matches 1153;   Mismatches   0;   Conservative   0;   Indels   1;   Gaps   0;

Qy   1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCGGGGCCGCC 60
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Qy   61 TGCCTGCCCCCAACAGCAGCGCGGCGCGCAGCTGGACGCGGCCCCCCGGCCCGACAGCGGC 120
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Qy   121 AGGCGCGGCTCGGAGGACGCGCAGCTGGAGCCGCACATCTCCCCGGCCATCCCGGTG 180
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Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTCGTCGGTCTGGTC 240
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Db   558 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTCGTCGGTCTGGTC 617

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTACATATTTAAC 300
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Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTTCACTTG 360
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Db   678 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTTCACTTG 737

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTACATATTTAAC 300
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Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTTCACTTG 360
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Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC 540
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Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCCGTCCTC 720
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Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
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Db   731 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 790

Qy   781 GGCTCCCGAGAAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
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Db   851 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 910

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCTCAGCTAGCTATACTTCTGCATCGCCTTAGGCTAT 960
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Db   911 AGCACCTCCCACAGCACAGCTGCTCTCTCTCAGCTAGCTATACTTCTGCATCGCCTTAGGCTAT 970

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
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Db   971 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1030

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC 1080
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Db   1031 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGCAGAGCACTAGCAGAGTC 1090

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1150

Qy   1141 TGACTAGTCGTGGA 1154
             ||||||||||||||
Db   1151 TGACTAGTCGTGGA 1164

RESULT 3
HUMOPRK1B
LOCUS   HUMOPRK1B   1604 bp   mRNA   linear   PRI 22-MAR-1995
DEFINITION Homo sapiens (clone d2-115) kappa opioid receptor (OPRK1) mRNA,
            complete cds.
ACCESSION   L37362
VERSION   L37362.1   GI:722617
KEYWORDS   OPRK1 gene; kappa opioid receptor; opioid receptor.

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Query Match          99.2%;    Score 1144.4;   DB 6;    Length 1182;
Best Local Similarity 99.5%;   Pred. No. 8.9e-201;
Matches 1148;  Conservative  0;  Mismatches   6;  Indels  0;  Gaps  0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGGGGAGGCGCGGAGGCCCTACCTGCGCCCCGAGCGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 ATGGAATCCCGATTCAGATCTTCCGGGGAGGCGCGGAGCCCTGGCCCTACCTGCGCCCCGAGCGCC 73

Qy     61 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGCGGTGGGCGCTGGGCCGCGCGACAGCAACGGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGCGGTGGGCGCTGGGCCGCGCGACAGCAACGGC 133

Qy    121 AGCGCCGGCTCGGAGACGCTGAGCGCCGCGCACATCTCCCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AGCGCCGGCTCGGAGACGCTGAGCGCCGCGCACATCTCCCGGCCATCCCGGTC 193

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTCGTGGGCAACTCGCTGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTCGTGGGCAACTCGCTGGTC 253

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAACCAACATTACATATTTAAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAACCAACATTACATATTTAAC 313

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTGTCGTTGGCATCTGTCAATAGTCCTTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTGTCGTTGGCATCTGTCAATAGTCCTTG 613

Qy    601 GTCAGGGAAGACGTGCATCATCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGTGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAAGACGTGCATCATCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGTGATGACTACTCC 673

Qy    661 TGGTGGGACCTTCTTCATGAAGATCTCGCTCTTGCCTTGCTTCATCTTGCCTTGCCTGTCTCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTTCTTCATGAAGATCTCGCTCTTGCCTTGCTTCATCTTGCCTTGCCTGTCTCTC 733

Qy    721 ATCATCATCCGTCTGCTACACCCTGATGATCCTGCGCTCCGTCTCAAGAGAGCGTCCGGCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 ATCATCATCCGTCTGCTACACCCTGATGATCCTGCGCTCCGTCTCAAGAGAGCGTCCGGCTCCTTTCT 793

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACTGCACCAGACTGGTTCCTGGTGGTGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACTGCACCAGACTGGTTCCTGGTGGTGTG 853

Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCCAGTCCATTCACATATTCTTCTTGATGAAAATTTCAAGCGGTGT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 GCGGTTTTCGTCGTCTGCTGGACTCCCGAATCCCATTCCCATTCACATATTCTTCTTGATGAAAACTTCAAGCGGTGT 913

Qy    901 AGCACCTCCACAGCACAGTCGCTCTCTCCAGCTATTACTTCTGCATCGCTATTACTTCTCGCATCGCCTTAGGCTAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AGCACCTCCACAGCACAGTCGCTCTCTCCAGCTATTACTTCTCGCATCGCTATTACTTCTCGCATCGCCTTAGGCTAT 973

Qy    961 ACCAACAGTAGCCTGAATCCATTCCTTCTTCTTAGTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 ACCAACAGTAGCCTGAATCCATTCCTTCTTCTTAGCGGTTTCTTGATGAAAACTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCGCACTAGCAGCAGAGTC 1080
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Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 857

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAATAGTCCTTGCAATAGTCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAATAGTCCTTGCAATAGTCATCAATATC 917

Qy    541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTGTCGTTGGCATCTGTCGTTGGCATCTGTCGAGGCACCAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    918 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTGTCGTTGGCATCTGTCGTTGGCATCTGTCGAGGCACCAA 977

Qy    601 GTCAGGGAAGACGTGCATGTCATTGAGTGTCTCCAGTAGTGACTGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    978 GTCAGGGAAGACGTCGAGTGTCATTGAGTGTCTCCAGTAGTCCCAGATGATGACTACTCC 1037

Qy    661 TGGTGGGACCTTCTTCATGAAGATCTCGGTCTTTGCCTTCATCTTGCCTTGCCTGTCTCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 TGGTGGGACCTTCTTCATGAAGATCTCGGTCTTTGCCTTCATCTTTGCCTTCCCTGTCCCTC 1097

Qy    721 ATCATCATCCGTCTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATCATCATCCGTCTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 1157

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACTGCGTAGGATCCGGTGGTGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAACTGCGTAGGATCCGGTGGTGTG 1217

Qy    841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCCATTCACATATTCATCACATATTCATCTGGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCCATTCACATATTCATCACATATTCATCTGGGGG 1277

Qy    901 AGCACCTCCACAGCACAGTCGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 AGCACCTCCACAGCACAGTCGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1337

Qy    961 ACCAACAGTAGCCTGAATCCATTCCTTCTTCTTCTTTCTTCTTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 ACCAACAGTAGCCTGAATCCATTCCTTCTTCTTCTTTCTTCTTCTCTACGCGGTGT 1397

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCGCAGAGAGTC 1457

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAAACCAGTA 1517

Qy   1141 TGACTAGTCGTGGA 1154
          |||||||||||||
Db   1518 TGACTAGTCGTGGA 1531
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RESULT 4
AR270854
LOCUS   AR270854   1182 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 1417 from patent US 6500938.
ACCESSION AR270854
VERSION   AR270854.1   GI:29702088
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 1182)
  AUTHORS Au-Young,J. and Seilhamer,J.J.
  TITLE   Composition for the detection of signaling pathway gene expression
  JOURNAL Patent: US 6500938-A 1417 31-DEC-2002;
FEATURES   Location/Qualifiers
  source   1..1182
           /organism="unknown"
           /mol_type="genomic DNA"
ORIGIN

Qy 481 TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db 494 TGCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy 541 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCTGAACAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 554 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCTGAACAGTCCTTGGAGGCACCAAA 613

Qy 601 GTCAGGGAGACGTCGATGTCATGAGTGCTCCTCCGCAGTGATGAGTGACTACTCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 614 GTCAGGGAGACGTCGATGTCATGAGTGCTCCTCCGCAGTGATGAGTGACTACTCC 673

Qy 661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGTGATCCCTGTCCTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 674 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGTCGTGATCCCTGTCCTC 733

Qy 721 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 734 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTGGTG 853

Qy 841 GCAGTCTTCGTCGTCTGGACTCCATTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 854 GCGGTTTTCGTCGTCTGGACTCCATTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 913

Qy 901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 914 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy 961 ACCAACAGTAGCCTGAATCCCATTCCTTCTTGATGAAAATTTCAAGCGGTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 974 ACCAACAGTAGCCTGAATCCCATTCCTTCTTGATGAAAATTTCAAGCGGTGT 1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy 1141 TGACTAGTCGTGGA 1154
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 6
LOCUS   AX774764   1182 bp   DNA   linear   PAT 09-JUL-2003
DEFINITION   Sequence 80 from Patent WO03038129.
ACCESSION   AX774764
VERSION   AX774764.1 GI:32486280
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Raponi,M.
  TITLE   Methods for assessing and treating leukemia
  JOURNAL   Patent: WO 03038129-A 80 08-MAY-2003;
             Ortho-Clinical Diagnostics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   99.2%; Score 1144.4; DB 6; Length 1182;

Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1093
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy 1141 TGACTAGTCGTGGA 1154
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 5
LOCUS   AX548862   1182 bp   DNA   linear   PAT 26-NOV-2002
DEFINITION   Sequence 147 from Patent WO02061087.
ACCESSION   AX548862
VERSION   AX548862.1 GI:25813740
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE   Antigenic peptides, such as for G protein-coupled receptors
             (GPCRs), antibodies thereto, and systems for identifying such
             antigenic peptides
  JOURNAL   Patent: WO 02061087-A 147 08-AUG-2002;
             Lifespan Biosciences, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1182
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   99.2%; Score 1144.4; DB 6; Length 1182;
Best Local Similarity   99.5%;
Matches 1148; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGACTCCCCATCCAGATCTTCCGCGGGAGCCGCGGCCTACCTGCCCCGAGCGGC 60
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Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGCGGCCTACCTGCCCCGAGCGGC 73

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGTTTCCCGGCTGGGCCGGAGCCGCAGCAGCAACGGC 120
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Db   74 TGCCTGCCCCCAACAGCAGCGGCCTGTTTCCCGGCTGGGCCGGAGCCGCAGCAGCAACGGC 133

Qy 121 AGCGCCGGCTCGGAGGACGCGCGAGCTGGAGCCCGCCGGCCATCTCCCCGGTC 180
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Db 134 AGCGCCGGCTCGGAGGACGCGCGAGCTGGAGCCCGCCGGCCATCCCCCGTC 193

Qy 181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db 194 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACACAACCAACATTTACATATTTAAC 300
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Db 254 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACACAACCAACATTTACATATTTAAC 313

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCCTTTCAGAGTACGGTCTACTTG 360
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Db 314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACATGCCCCTTTCAGAGTACGGTCTACTTG 373

Qy 361 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTGTAAGATAGTAATTTCCATTGATTACTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 374 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTGTAAGATAGTAATTTCCATTGATTACTAC 433

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 493

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Db   1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGATGGAGCCGGCAGAGCACTAGCAGAGTC 1093
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Qy   1081 CGAAATACAGTTCAGGATCCTGCTTCACCTGAGGGGACTGCTTGCCTTCTGAGGTGGGAGGCTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCCTGCTTCACCTGAGGGGACCATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1154 TGACTAGTCGTGGA 1167
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RESULT 7
HSU11053
LOCUS   HSU11053   1182 bp   mRNA   linear   PRI   22-AUG-1994
DEFINITION Human kappa opioid receptor (hKOR) mRNA, complete cds.
ACCESSION   U11053
VERSION   U11053.1 GI:532059
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1182)
  AUTHORS   Mansson,E., Bare,L. and Yang,D.
  TITLE   Isolation of a human kappa opioid receptor cDNA from placenta
  JOURNAL   Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
  MEDLINE   94338360
   PUBMED   8060324
REFERENCE   2 (bases 1 to 1182)
  AUTHORS   Mansson,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,
            PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA
FEATURES   Location/Qualifiers
     source   1..1182
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                     /clone="phK1.3"
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     gene   1..1182
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     CDS   14..1156
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                     /codon_start=1
                     /product="kappa opioid receptor"
                     /protein_id="AAA20985.1"
                     /db_xref="GI:532060"
                     /translation="MESPIQIFRGEPGPTCAPSACLPNSSAWFPGWAEPDSNGSAGS
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                     CHPVKALDFRTPLKAKIINICIWLLSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                     YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                     LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                     ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"

ORIGIN
Query Match   99.2%;   Score 1144.4;   DB 9;   Length 1182;
Best Local Similarity 99.5%;   Pred. No. 8.9e-201;
Matches 1148;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGGCGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 133

Qy  121 AGGCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 AGGCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 193
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Qy    1 ATGGACTCCCGATCCAGATCTTCCGGCGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC 60
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Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCGACAGCAACGGC 133

Qy  121 AGGCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 AGGCCGGCTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCCCGGCCATCCCGGTC 193

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC 240
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Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTACATATTAAC 300
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Db  254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTACATATTAAC 313

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGATACGGTCTACTTG 360
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Db  314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGATACGGTCTACTTG 373

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Db  374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 480
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Db  434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 493

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Qy  541 TGCATCTGGCTGCTCTCGTCGGTCATCGGTGGCATCGTCAATAGTCCTTGGAGGCACCAAA 600
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Db  554 TGCATCTGGCTGCTCTCGTCGGTCATCGGTGGCATCGTCAATAGTCCTTGGAGGCACCAAA 613

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
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Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
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Db  674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 733

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTCTCT 780
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Db  734 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTCTCT 793

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db  794 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy  841 GCAGTTTTCGTCGTGTGCTGGACTCCCATCCATTCACATATTCTGGTGGAGGCTCTGGGG 900
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Qy  901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Db  914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
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Db  974 ACCAACAGTAGCCTGAATCCCATTCTTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGATGGAGCCGGCAGAGCACTAGCAGAGTC 1080
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ACCESSION   AR281679
VERSION   AR281679.1 GI:29717434
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1143)
  AUTHORS   ConKlin,B.R.
  TITLE   Selective target cell activation by expression of a G
             protein-coupled receptor activated superiorly by synthetic ligand
  JOURNAL   Patent: US 6518480-A 1 11-FEB-2003;
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   98.9%; Score 1141.4; DB 6; Length 1143;
Best Local Similarity 99.9%; Pred. No. 3.2e-200;
Matches 1142; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGAGCCGGCCCTACCTGCGGGCCCGAGCGGCC   60
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Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGAGCCGGCCCTACCTGCGGGCCCGAGCGGCC   60

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCGGCCGCAGCGGCCCGGTTCCCGGCGTGGCGCGAGCAGCAGCGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGGCCGGCCGCAGCGGCCCGGTTCCCGGCGTGGCGCGAGCAGCAGCGGC 120

Qy 121 AGCGCCGGCTCGGAGGACGGCAGCTGGGCGCGCACATCTCCCCGGCCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGCGCCGGCTCGGAGGACGGCAGCTGGGCGCGCACATCTCCCCGGCCATCCCGGTC 180

Qy 181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTGGTGGCAACTCGCTCGGTC 240
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Db 181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTGGTGGCAACTCGCTCGGTC 240

Qy 241 ATGTTCGTGATCATCCGATACACAACAGACAAAGATGAAGACAGCAGCAGCAGCACCATGAACATTTACATATTTAAC 300
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Db 241 ATGTTCGTGATCATCCGATACACAACAGACAAAGATGAAGACAGCAGCAGCAGCACCATGAACATTTACATATTTAAC 300

Qy 301 CTGGCTTTGGCAGATGCTTTGGGGATGTGCTTGCAAGATAGTAATTCCATTGATTACTAC 360
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Db 301 CTGGCTTTGGCAGATGCTTTGGGGATGTGCTTGCAAGATAGTAATTCCATTGATTACTAC 360

Qy 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAATGAAGGCAAAGACCATCAATATC 420
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Db 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAATGAAGGCAAAGACCATCAATATC 420

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCTTCCGCACACCCTTCTGCAAGATAGTCCTTGGAGGCACCAAA 480
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Db 421 AACATGTTCACCAGCATCTTCACCTTGACCTTCCGCACACCCTTCTGCAAGATAGTCCTTGGAGGCACCAAA 480

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCTGCAAGATCATCAATATC 540
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Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCTGCAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTGTCGTCAATCTCTTGCAATAGTCCTTGGAGGCACCAAA 600
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Db 661 TGGTGGGACCTTCATGAAGATCTCGGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720

Qy 721 ATCATCATCGTCTACACACCCTGATGATCCGTCTGCGTCTCAAGAGCGTCAAGATCC 780
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Db 721 ATCATCATCGTCTACACACCCTGATGATCCGTCTGCGTCTCAAGAGCGTCAAGATCC 780

Qy 181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTTGGTGGCAACTCGCTCGGTC   240
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Db 194 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTTGGTGGCAACTCGCTCGGTC   253

Qy 241 ATGTTCGTGATCATCCGATACACAACAGATGAAGACAGCAGCAGCAACATTTACATATTTAAC   300
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Db 254 ATGTTCGTGATCATCCGATACACAACAGATGAAGACAGCAGCAGCAACATTTACATATTTAAC   313

Qy 301 CTGGCTTTGGCAGATGCTTTAGTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 314 CTGGCTTTGGCAGATGCTTTAGTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG   373

Qy 361 ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTCGTGTCAAGATAGTAATTCCATTGATTACTAC   420
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Db 374 ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTCGTGTCAAGATAGTAATTCCATTGATTACTAC   433

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG   480
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Db 434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG   493

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCTGCAAGGCAAAGATCATCAATATC   540
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Db 494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTCTGCAAGGCAAAGATCATCAATATC   553

Qy 541 TGCATCTGGCTGCTGTCGTCAATCTCTTGCAATAGTCCTTGGAGGCACCAAA   600
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Db 554 TGCATCTGGCTGCTGTCGTCAATCTCTTGCAATAGTCCTTGGAGGCACCAAA   613

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   660
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Db 614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   673

Qy 661 TGGTGGGACCTTCATGAAGATCTCGGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC   720
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Db 674 TGGTGGGACCTTCATGAAGATCTCGGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC   733

Qy 721 ATCATCATCGTCTGCTACACCCTGATGATCCGGCTCAAGAGCGTCCGGCTCCGGCTCCTTTCT   780
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Db 734 ATCATCATCGTCTGCTACACCCTGATGATCCGGCTCAAGAGCGTCCGGCTCCGGCTCCTTTCT   793

Qy 781 GGCTCCGAGAGAAAGATCGCAACCTGCTAGGATCACCACAGGATCTGGTCCTGGTGGTGTG   840
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Db 794 GGCTCCGAGAGAAAGATCGCAACCTGCTAGGATCACCACAGGATCTGGTCCTGGTGGTGTG   853

Qy 841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGGTGGAGGCTCTGGGG   900
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Db 854 GCGGTTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTCGGTGGAGGCTCTGGGG   913

Qy 901 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCGAGGACATCGAATCCGCCTTAGGCTAT   960
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Db 914 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCGAGGACATCGAATCCGCCTTAGGCTAT   973

Qy 961 ACCAACAGTAGCCTGAATCCCATTCTTCTTGATGAAAATTCAAGCGGTGT   1020
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Db 974 ACCAACAGTAGCCTGAATCCCATTCTTCTTGATGAAAACTTCAAGCGGTGT   1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGCGCAGAGCACTAGCAGAGTC   1080
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Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGCGCAGAGCACTAGCAGAGTC   1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGAATGGAATAAACCAGTA   1140
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Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGAATGGAATAAACCAGTA   1153

Qy 1141 TGACTAGTCGTCGGA   1154
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Db 1154 TGACTAGTCGTCGGA   1167

RESULT 8
AR281679
LOCUS   AR281679   1143 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6518480.

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Qy    61 TGCCTGCCCCCAACAGCAGCCGCCTGGTTCCCGGCCTGGGCCTGGGCCCAGCAGCAACGGC 120
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Qy   121 AGGCGCGGCTCGGAGGAGACGCGCAGCTGGCGGAGCCCCGCCGCCACATCTCCCCGGCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGGCGCGGCTCGGAGGAGACGCGCAGCTGGCGGAGCCCCGCCGCCACATCTCCCCGGCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTGAAGGCAAAGATCATCAATATC 540
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Db   541 TGCATCTGGCTGCTGTCGTCGTCATCTGTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

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Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTAAGAGCGTCCGCTCCTTCT 780
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Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCAGAGACTGGTCCTGGTGGTGGTG 840
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Qy   901 AGCACCTCCCACAGCACACAGCTGCTCTCTCCACCTACGCCTTTCTGATGAAACTTCAAGCCGGTGT 960
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Qy  1141 TG 1142
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Db  1141 TG 1142
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RESULT 9

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A48343
LOCUS       A48343              1142 bp    DNA     linear     PAT 07-MAR-1997
DEFINITION  Sequence 1 from Patent WO9601898.
ACCESSION   A48343
VERSION     A48343.1    GI:2302133
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1  (bases 1 to 1142)
AUTHORS     Kieffer,B. and Simonin,F.
TITLE       HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
JOURNAL     Patent: WO 9601898-A 1 25-JAN-1996;
            UNIV PASTEUR (FR)
COMMENT     Other publication FR 2722209 960112.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match   98.8%; Score 1140.4; DB 6; Length 1142;
Best Local Similarity   99.9%; Pred. No. 4.9e-200;
Matches 1141; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Db     1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGAGCCGGCCCACCTGCGCCCCC 60
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Db   1141 TG 1142

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Db        1141  TG 1142

RESULT 10
AR141371
LOCUS         AR141371              1142 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION    Sequence 1 from patent US 6146835.
ACCESSION     AR141371
VERSION       AR141371.1  GI:15100887
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 1142)
  AUTHORS     Kieffer,B. and Simonin,F.
  TITLE       Human kappa opioid receptor, nucleic acids and uses thereof
  JOURNAL     Patent: US 6146835-A 1 14-NOV-2000;
FEATURES             Location/Qualifiers
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                 /organism="unknown"
                 /mol_type="unassigned DNA"
ORIGIN

Query Match        98.8%;  Score 1140.4;  DB 6;  Length 1142;
Best Local Similarity  99.9%;  Pred. No. 4.9e-200;
Matches 1141;  Conservative    0;  Mismatches   0;  Indels    1;  Gaps    0;

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Db     61  TGCCTGCGCCCCCAACAGCAGCCGGCCTGGTTCCCGGGCTGGGGCCGAGCCGACAGCAACGGC  120

Qy    121  AGCGCCCGCTCCGAGGACGCGGCCAGCTCGAGCCATCCCGGCCGGTC  180
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Db    121  AGCGCCCGCTCCGAGGACGCGGCCAGCTCGAGCCATCCCGGCCGGTC  180

Qy    181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC  240
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Db    181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC  240

Qy    241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCCAACATTTACATATTTAAC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCCAACATTTACATATTTAAC  300

Qy    301  CTGGCCTTTGGCAGATGCTTTAGTACTACAACACCATGCCCTTTCAGAGTACGGTCTACTTG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CTGGCCTTTGGCAGATGCTTTAGTACTACAACACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy    361  ATGAAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTGCTGTGCAAGATTACATCATGATTACTAC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATGAAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTGCTGTGCAAGATTACATCATGATTACTAC  420

Qy    421  AACATGTTCACCAGCATCTTCACCTTGGACCGTGGACCGCTACATTGCCGTG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AACATGTTCACCAGCATCTTCACCTTGGACCGTGGACCGCTACATTGCCGTG  480

Qy    481  TGCCACCCGTGAAGGCTTTGAAGGCTTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TGCCACCCGTGAAGGCTTTGAAGGCTTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy    541  TGCATCTGGCTGCTGTCGTCGTCCAATAGTCCTTGCAATCTCGTGGCATCTCGTGGCATCTCTGCAATAGTCCTTGCAATAGTCCTTGGAGGCACCAAA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TGCATCTGGCTGCTGTCGTCGTCCAATAGTCCTTGCAATCTCGTGGCATCTCGTGGCATCTCTGCAATAGTCCTTGCAATAGTCCTTGGAGGCACCAAA  600

Qy    601  GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GTCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC  660

Qy    661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720

Qy    721  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTCTTTCT  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTCTTTCT  780

Qy    781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCGTGGTGGGTG  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCGTGGTGGGTG  840

Qy    841  GCAGTCTTCGTCGTCTTCGTCGGACTCCATTCACATATTCATCATCCTGGTGAGGCTCTGGGG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCAGTCTTCGTCGTCTTCGTCGGACTCCATTCACATATTCATCATCCTGGTGAGGCTCTGGGG  900

Qy    901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTATTCTTGCATCGCATCGCCTTAGGCTAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTATTCTTGCATCGCATCGCCTTAGGCTAT  960

Qy    961  ACCAACAGTAGCCTGAATCCCATTCTTCACGGCCTTCTTGATGAAAATTCAAGCGGTGT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  ACCAACAGTAGCCTGAATCCCATTCTTCACGGCCTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy   1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080

Qy   1081  CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAAATACAGTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141  TG 1142
           ||
Db   1141  TG 1142

RESULT 11
AF498922
LOCUS         AF498922               1143 bp    mRNA    linear   PRI 01-MAY-2002
DEFINITION    Homo sapiens opioid receptor kappa (OPRK1) mRNA, complete cds.
ACCESSION     AF498922
VERSION       AF498922.1  GI:20379019
KEYWORDS      .
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 1143)
  AUTHORS     Puhl,H.L., Ikeda,S.R. and Aronstam,R.S.
  TITLE       Direct Submission
  JOURNAL     Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
              Institute, One Guthrie Square, Sayre, PA 18840, USA
FEATURES             Location/Qualifiers
     source      1..1143
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /tissue_type="brain"
     gene        1..1143
                 /gene="OPRK1"
     CDS         1..1143
                 /gene="OPRK1"
                 /note="G protein coupled receptor"
                 /codon_start=1
                 /product="opioid receptor kappa"
                 /protein_id="AAM21070.1"
                 /db_xref="GI:20379020"
                 /translation="MESPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
                 EDAQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIRYTKMKTATNIYIFNLA
                 LADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYNMFTSIFTLTMMSVDRYIAV
                 CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
                 YSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITRLV
                 LVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLD
                 ENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPAYLRDIDGMNKPV"
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ORIGIN

Query Match   98.6%;   Score 1138.2; DB 9; Length 1143;
Best Local Similarity 99.7%;   Pred. No. 1.2e-199;
Matches 1140; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAATCCCGATTCAGATCTTCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGGC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGTCTGGGCCGGAGCCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGC 120

Qy    121 AGCGCCGGCTCGGAGGACGGGCCGCAGCTGGACGCGCCACATCTCCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGCGCGGCTCGGAGGACGGGCCGCAGCTGGAGCCCCGGCCACATCTCCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db    181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
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Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGCTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTGGGGATGCTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACACCGTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACACCGTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGCTTTGGACTTCCGACACACCCTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGCTTTGGACTTCCGACACACCCTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTATCTCGTGTGACATCTCGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTATCTCGTGTGACATCTCGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTGCAATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTGCAATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTCGTGCGTCCTTCATCTTTGCCTTCGTCTTCATCTTTGCCTTCGTCTCCGTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTTCGTGCGTCCTTCATCTTTGCCTTCGTCTTCATCTTTGCCTTCGTCTCCGTC 720

Qy    721 ATCATCATCGTCTGCTACACCCTGCGTAGGATCACCACAGACTGTCCGGTCTGGTGGTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGCGTAGGATCACCACAGACTGTCCGGTCTGGTGGTG 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCCTGGTGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCTCCTGGTGTGGTG 840

Qy    841 GCAGTCTTCGTCGTCTGCTGCTGGACTCCCATTCATCCTGGTGGAGGCTCGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTCGTCTGCTGCTGACTCCCATTCATCCTGGTGGAGGCTCTGGGG 900

Qy    901 AGACCTTCCACAGCAGCAGTCTGCTCTCTTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTTCCACAGCAGCAGTCTGCTCTCTTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGGCTGGAATCCCATTCTTCTACGCCTTTCTGATGAAATTCAAGCCGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGGCTGGAATCCCATTCTTCTACGCCTTTCTGATGAAAACTTCAAGCCGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1080
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Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGA 1143
          |||
Db   1141 TGA 1143
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RESULT 12
AR281680
LOCUS   AR281680   1284 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6518480.
ACCESSION   AR281680
VERSION   AR281680.1 GI:29717435
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1284)
  AUTHORS   Conklin,B.R.
  TITLE   Selective target cell activation by expression of a G
            protein-coupled receptor activated superiorly by synthetic ligand
  JOURNAL   Patent: US 6518480-A 3 11-FEB-2003;
FEATURES   Location/Qualifiers
     source   1..1284
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN

Query Match   98.5%;   Score 1136.2; DB 6; Length 1284;
Best Local Similarity 99.7%;   Pred. No. 2.9e-199;
Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCCT 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 TCGACTCCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCGAGCGCCT 172

Qy     62 GCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGCA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 GCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCTGGGCCGGAGCCCGACAGCAACGGCA 232

Qy    122 GCGCCGGCTCGGAGGACGGGCCGCAGCTGGAGCCGCCGCCGCCACATCTCCCGGCCATCCCGGTCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 GCGCCGGCTCGGAGGACGGGCCGCAGCTGGAGCCGCCGCCGCCACATCTCCCGGCCATCCCGGTCA 292

Qy    182 TCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTCA 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTCA 352

Qy    242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAACC 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAACC 412

Qy    302 TGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTGA 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 TGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGAGTACGGTCTACTTGA 472

Qy    362 TGAATTCCTGGCCTTTTGGGGATGCTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    473 TGAATTCCTGGCCTTTTGGGGATGCTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 532

Qy    422 ACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCCGCTACATTGCCGTGT 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 ACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCCGCTACATTGCCGTGT 592

Qy    482 GCCACCCCGTGAAGGCTTTGGACTTCCGACACCCTTGAAGGCAAAGATCATCAATATCT 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Matches 1135; Conservative 0; Mismatches 0; Indels 8; Gaps 0;

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Qy      1 ATGGACTCCGATCCAGATCTTCCGGGGAGCCGGCGGCCCTACTGCGCCCCGAGCGCC   60
          ||||| |||||||||||||||||||||||| | | ||||||||||||||||||||||||
Db      1 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCCTACTGCGCCCCGAGCGCC   60

Qy     61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCGTCGGCTGGCTGGCCCGACAGCAACGGC  120
          |||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGCGTCGGCTGGCTGGCCCGACAGCAACGGC  120

Qy    121 AGGGCCGGCTCGGAGGACGCGCAGCTGAGACCCGCGCACATCTCCCCGGCCATCCGGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGGCCGGCTCGGAGGACGCGCAGCTGAGACCCGCGCACATCTCCCCGGCCATCCGGTC  180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTCGTCGGTGGGCAACTCGCTGGTC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTCGTCGGTGGGCAACTCGCTGGTC  240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCGAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGTGTCAAGATAGTAATTTCCATTGATTACTAC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGTGTCAAGATAGTAATTTCCATTGATTACTAC  420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTGCACATTGCCGTG  480
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Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACGCTGCACATTGCCGTG  480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCATCTGGCTGGTCGTGCATCGTCGTGGCATCTCTGCGCAATAGTCCTTGAAGGCAAAGATCATCAATATC  540

Qy    541 TGCATCTGCTGGTCGTGTCGTCATCGTTGCGTGATGTCATTGAGTCGTCCTTGCAGTGACTACTCC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGCTGGTCGTGCTGTCATCGTTGCGATCTGCGCAATAGTCCTTGCAGTGACTACTCC  600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCCTTGCGGTCTTCGTCATCTTTGCCTTCGTCATCTCGTCCTC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCCTTGCGGTCTTCGTCATCTTTGCCTTCGTCATCTCGTCCTC  660

Qy    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCAAGAGCGTCCGGCTCCTTTCT  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCAAGAGCGTCCGGCTCCTTTCT  720

Qy    721 ATCATCATCGTCTGCTACCACCCTGATGATCCTGCGTCTCAAGAGCGTCGGTCCTGGTCCTGGTGGTGGTG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACCACCCTGATGATCCTGCGTCTCAAGAGCGTCGGTCCTGGTCCTGGTGGTGGTG  780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCAACAAGAGACTGGTCCTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCAACAAGAGACTGGTCCTGGTGGTGGTG  840

Qy    841 GCAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGGTTTCGTCTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGG  900

Qy    901 AGACCTCCCACAGCACAGCTGTCTTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGACCTCCCACAGCACAGCTGTCTTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy    961 ACCAACAGTAGCCTGGAATCCGAATCCATTCCTCTACGCCTTTCTTGATGAAATTTCAAGCGGTGT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGGAATCCGAATCCATTCCTCTACGCCTTTCTTGATGAAATTTCAAGCGGTGT  1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCGGCACTAGCAGAGTC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCGGCACTAGCAGAGTC  1080
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Db    593 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCT  652

Qy    542 GCATCTGCTGGTCGTCATCGTTGCGTGATGTCATTGAGGCACCAAAG  601
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GCATCTGCTGGTCGTCGTCATCGTTGCGATCTGCGCAATAGTCCTTGAGGCACCAAAG  712

Qy    602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCCTTGCAGTTCCCAGATGATGACTACTCCT  661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 TCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCCTTGCAGTTCCCAGATGATGACTACTCCT  772

Qy    662 GGTGGGACCTTCTGCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCCTCA  721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 GGTGGGACCTTCTGCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTCCTCA  832

Qy    722 TCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCTTTCTG  781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 TCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCTTTCTG  892

Qy    782 GCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCAACAAGAGACTGGTCCTGGTGGTGGTGG  841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 GCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCAACAAGAGACTGGTCCTGGTGGTGGTGG  952

Qy    842 CAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGGA  901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CAGTCTTCGTCTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTCGGGGA  1012

Qy    902 GCACCTCCCACAGCACAGCTGTCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA  961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 GCACCTCCCACAGCACAGCTGTCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA  1072

Qy    962 CCAACAGTAGCCTGAATCCGATCCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTCC  1021
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 CCAACAGTAGCCTGAATCCGATCCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTCC  1132

Qy   1022 TCCGGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTCC  1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 TCCGGGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCAGAGCACTAGCAGAGTCC  1192

Qy   1082 GAAATACAGTTCAGGATCCTGCTTACCTGGGGACATCGATGGGATGAATAAACCAGTAT  1141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 GAAATACAGTTCAGGATCCTGCTTACCTGGGGACATCGATGGGATGAATAAACCAGTAG  1252

Qy   1142 G  1142
          |
Db   1253 G  1253
```

RESULT 13
AX280919

LOCUS   AX280919   1143 bp   DNA   linear   PAT 02-NOV-2001
DEFINITION Sequence 542 from Patent WO0177172.
ACCESSION   AX280919
VERSION   AX280919.1 GI:16608215
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.
  TITLE   Non-endogenous, constitutively activated known g protein-coupled
            receptors
  JOURNAL   Patent: WO 0177172-A 542 18-OCT-2001;
            Arena Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1143
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   97.9%; Score 1130.2; DB 6; Length 1143;
Best Local Similarity   99.3%; Pred. No. 3.7e-198;

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Qy   495 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 554
                                                                         
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGGTGTGTCGCAGAGATAGTAATTCCATTGATTACTAC 420
             ||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140

Db   555 ATGAATTCCTGGCCTTTTGGGGATGGTGTGTCGCAAGATAGTAATTCCATTGATTACTAC 614

Qy  1141 TGA 1143
         |||
Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTGACATTGCCGTG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   615 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTGACATTGCCGTG 674

Db  1141 TGA 1143

RESULT 14
AY168006
LOCUS       AY168006           1396 bp    mRNA    linear   PRI 25-DEC-2002
DEFINITION  Homo sapiens DRG kappa 1 splice variant KOR 1A mRNA, complete cds,
            alternatively spliced.
ACCESSION   AY168006
VERSION     AY168006.1  GI:27373027
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1396)
  AUTHORS   Lu,L.L. and Mansson,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371
            Phoenixville Pike, Malvern, PA 19355, USA
FEATURES             Location/Qualifiers
     source          1..1396
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             237..1337
                     /note="opioid receptor kappa 1A; alternatively spliced"
                     /codon_start=1
                     /product="DRG kappa 1 splice variant KOR 1A"
                     /protein_id="AAN87342.1"
                     /db_xref="GI:27373028"
                     /translation="MDSPIQIFRGEPGPTCAPSACLPPNSSAGSEDAQLEPAHISPAI
                     PVITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQS
                     TVYLMNSWPFGDALCKIVISIDYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLK
                     AKINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWNDLFMKICVFI
                     FAFVIPVLIIIVCYTLMIRLKSVRLLSGSREKDRNLRRITRLVVVAVFVCWTPI
                     HIFLIVEALGSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPL
                     KMRMERQSTSRVRNTVQDDPAYLRDIDGMNKPV"

ORIGIN
Query Match     91.6%;  Score 1056.8;  DB 9;  Length 1396;
Best Local Similarity   96.2%;  Pred. No. 1.2e-184;
Matches 1110; Conservative    0; Mismatches    2; Indels   42; Gaps    1;

Qy     1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCGC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   237 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC 296

Qy    61 TGCCTGCCCCCCAAACAGCAGGCGCCTGGTTTCCCGGCCGAGCCCGACAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   297 TGCCTGCCCCCCAACA-------------------------------------GC 314

Qy   121 AGCGGCCGGCTCGGGAGGACGCGGAGCCGCAGCTGGAGGACCGCCGCACATCTCCCCGGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 AGCGGCCGGCTCGGGAGGACGCGGAGCCGCAGCTGGAGGACCGCCGCACATCTCCCCGGTC 374

Qy   181 ATCATCACGGCGCGGTCTACTCCGGTCGTTCGTCGTCGTTCGTCGTCGTTCGTCGGCTGGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   375 ATCATCACGGCGCGGTCTACTCCGGTCGTTCGTCGTTCGTCGTCGTTCGTCGGCAACTCGGC 434

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACCAATTTACATATTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACCAACATTTACATATTAAC 494

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
         |||||||||||||||||||||||
```

RESULT 15
AR281681
LOCUS   AR281681   1275 bp   DNA   linear   PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6518480.
ACCESSION   AR281681
VERSION   AR281681.1 GI:29717436
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1275)
  AUTHORS   Conklin,B.R.
  TITLE   Selective target cell activation by expression of a G
            protein-coupled receptor activated superiorly by synthetic ligand

```
Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   675 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC 734

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   735 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 794

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   795 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 854

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTTGTCGTGATCCCGTCCTC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   855 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTTGTCGTGATCCCGTCCTC 914

Qy   721 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAAGAGGGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   915 ATCATCATCGTCTGCTACACCCTGATGATCCGTCTCAAGAGCGTCCGGCTCCTTTCT 974

Qy   781 GGCTCCCGAGAGAAAGATGCCAACTGCTGGTAGGATCACCAGACTGGTCCTGGTGGTGTG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   975 GGCTCCCGAGAGAAAGATGCCAACTGCTGGTAGGATCACCAGACTGGTCCTGGTGGTGTG 1034

Qy   841 GCAGTTCGTGTCGTGGTGGACTCCCATTCACATATTCATCCTGGTGGAGGCCTTAGGCTAT 900
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Db  1035 GCAGTTCGTGTCGTGGTGGACTCCCATTCACATATTCATCCTGGTGGAGGCCTTAGGCTAT 1094

Qy   901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1095 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1154

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1155 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1214

Qy  1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1215 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1274

Qy  1081 CGAAATACAGTTCAGGATCCTTACCTGCTTACCTGCTTACCTGAGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1275 CGAAATACAGTTCAGGATCCTTACCTGCTTACCTGCTTACCTGAGGGATGAATAAACCAGTA 1334

Qy  1141 TGACTAGTCGTGGA 1154
         ||||||||||||||
Db  1335 TGACTAGTCGTGGA 1348
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JOURNAL    Patent: US 6518480-A 5 11-FEB-2003;
FEATURES
     source        1..1275
                   /organism="unknown"
                   /mol_type="genomic DNA"
ORIGIN

Query Match          86.6%;  Score 999.4;  DB 6;  Length 1275;
Best Local Similarity 93.0%;  Pred. No. 4.6e-174;
Matches  1061;  Conservative    0;  Mismatches   71;  Indels    9;  Gaps    1;

Qy      2 TGGACTCCCGATCCAGATCTTCGCGGGAGCCGGCCTACTTGCCCCCGAGCGCCT 61
          ||||||||||||||||||| |||||||||||||||||||||||||| |||||||||
Db    113 TCCACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCTACTTGCCCCGCCCAGCGCCT 172

Qy     62 GCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCTCGGCGCCGAGCCCGACAGCAACGGCA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 GCCTGCCCCCAACAGCAGCGGCTGGTTCCCGGCTCGGCGCCGAGCCCGACAGCAACGGCA 232

Qy    122 GGGCCCGGCTCGGAGGACGCGCAGCTGGACGCCCGGCCACATCTCCCCGGCCATCCCGGTCA 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 GCGCCCGGCTCGGAGGACGCGCAGCTGGACGCCCGGCCACATCTCCCCGGCCATCCCGGTCA 292

Qy    182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGGCTTGGTGGGCAACTCGCTGGTCA 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTCGGCTTGGTGGGCAACTCGCTGGTCA 352

Qy    242 TGTTCGTGATCATCCGATACACAAAGATGAACAGCAGCAACCAACATTTACATATTTAACC 301
          |||||||||||||||||||| |||||||||||||||||||||||||||| |||||||||
Db    353 TGTTCGTGATCATCCGATACACAAAGATGAACAGCAACCAACATTTACATATTTAACC 412

Qy    302 TGGCTTTGGCAGATGCTTAGTTACTACAACCATGTGCTGTCAAGATAATTTCCATTGATTACTACA 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 TGGCTTTGGCAGATGCTTAGTTACTACAACCATGTGCTGTCAAGATTGTCATTTCCATTGACTACTACA 472

Qy    362 TGAATTCCTGGCCTTTTGGGGATGTGTCTGCAAGATAGTAATTTCCATTGATTACTACA 421
          ||||||||| ||| |||||||||||||||||||||||||| |||| ||||||||||||
Db    473 TGAATTCCTGGCCTTTTGGGATGTTCTGTGTGCAAGATTGTCATTTCATTGACTACTACA 532

Qy    422 ACATGTTCACCAGCATCTCACCTTGACCATGAGAGCGGTGACACCGCTACATTGCCGTGT 481
          |||||||| |||||||||| |||||||||||||||||||||| |||||||||||||||
Db    533 ACATGTTTACCAGCATATTACCTTGACCATGAGGATGAGGTGGACCGTTACATTGCCGTGT 592

Qy    482 GCCACCCGTGAAGGCTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT 541
          |||||||||||||||||||| |||| |||||||||||||||||||||||||||||||
Db    593 GCCACCCGTGAAAGCTTGGATTTCCGGATTTCCGAACACCTTTGAAAGCAAAGATCATCAACATCT 652

Qy    542 GCATCTGCTGTCGTCATCTTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCCAAAG 601
          |||| ||| ||| ||| |||||||| ||| |||||| |||||||| ||| |||||||
Db    653 GCATTTGGCTACTGGCATCATCTGTTGGTATATCAGCCATAGTCCTTGGGGGTGACCCAAAC 712

Qy    602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT 661
          ||||| ||||| ||| |||||||||||||||||||| ||||||||||||||||||
Db    713 CCCGGGATGGAGCAGTGTATGCACGCTCACGCTCCAGCC--------CAGTCTGGT 763

Qy    662 GGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCA 721
          |||| ||||| |||||||||||| |||||||||||| |||||||||||||||||||||
Db    764 ACTGGGACACTGTGACCAAGATCGCGGTCGTTCATCTTTGCCTTCGTGATCCCTGTCCTCA 823

Qy    722 TCATCATCGTCTGTACACCCTGCTGATGATCTCGGTCTCAAAGAGCGTCCGGCTCCTTTCTG 781
          ||||||||||| |||||||| |||| |||||| ||||||||||||||||||||||||||
Db    824 TCATCATCGTCTGTACACCCGGCATCCGTGATGATCTCAAAGAGCGTCCGGCTCCTTTCTG 883

Qy    782 GCTCCCGAGAAAAGATCTGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGTGG 841
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 GCTCCCGAGAAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGTGG 943

Qy    842 CAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA 901
          |||||||||||||||||||||||||| |||| |||||||||||||||||||||||||
Db    944 CAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA 1003

Qy    902 GCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 GCACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATA 1063

Qy    962 CCAACAGTAGCCTGAATCCCATTCTCTTACGCCTTTCTTGATGAAAATTTCAAGCGGTGTT 1021
          |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Db   1064 CCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT 1123

Qy   1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCAGAGCACTAGCAGAGTCC 1081
          ||||||||||||||||||||||||||||||||             |||||||||||||||||||||
Db   1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTCC 1183

Qy   1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGAATAAACCAGTAT 1141
          ||||||||||||||||||||||||||||||||||                |||||||||||||
Db   1184 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAG 1243

Qy   1142 G 1142
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Db   1244 G 1244


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               GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

QM nucleic - nucleic search, using sw model

Run on:   April 6, 2005, 12:28:42 ; Search time 700.667 Seconds
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Perfect score:  1154
Sequence:       1 atggactcccgatccagat.........ccagtatgactagtcgtgga 1154

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:        8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1150.8	99.7	1154	12	ADN30506	Human kap
5	1150.8	99.7	1154	12	ADN30510	Human kap
6	1150.8	99.7	1154	12	ADN30507	Human kap
7	1150.8	99.7	1154	12	ADN30511	Human kap
8	1150.8	99.7	1154	12	ADN30509	Human kap
9	1144.4	99.2	1182	8	AB242678	Human opi
10	1144.4	99.2	1182	10	AAD58490	Human kap
11	1144.4	99.2	1182	10	ADE84861	Farnesyl
12	1144.4	99.2	1182	10	ACA56819	Human sig
13	1144.4	99.2	1182	12	ADI56615	Human pol
14	1141.4	98.9	1143	2	AAT90998	Human kap
15	1140.4	98.8	1142	2	AAT12550	Human kap
16	1136.2	98.5	1284	2	AAT90999	Human kap
17	1136.2	98.5	1284	11	ADI90106	cDNA enco
18	1133.4	98.2	1143	12	ADO30011	Human GPC
19	1130.2	97.9	1143	5	ABI98011	Non-endog
20	999.4	86.6	1275	2	AAT92601	Human kap
21	999.4	86.6	1275	11	ADL90108	Human kap
22	994.6	86.2	1275	11	ADL90110	Human kap
23	979.4	84.9	1875	11	ADL90116	Human kap
24	963.4	83.5	1875	11	ADL90118	Human kap
25	909.2	78.8	1408	2	AAV49254	Mouse kap
26	909.2	78.8	1410	2	AAQ75926	Mouse kap
27	909.2	78.8	1410	13	ADR44860	Mouse kap
28	909.2	78.8	2481	13	AAQ86725	Mammalian
29	909.2	78.8	2481	13	ADR44862	Rat kappa
30	898.2	77.8	1143	12	ADO30301	Mouse GPC
31	877.8	76.1	1911	11	ADL90120	Human kap
32	868	75.2	1000	2	AAQ75931	Human kap
33	446.4	38.7	2135	5	AAF85416	Nucleotid
34	444.8	38.5	1401	13	ADR44848	Rat mu-op
35	444.8	38.5	1618	2	AAQ89222	Rat mu op
36	444.8	38.5	1618	2	AAQ89223	Transcrip
37	444.8	38.5	1618	3	AAS9499	cDNA enco
38	441.8	38.3	2070	2	AAQ79199	Rat mu-su
39	436.8	37.9	9426	13	ADR44835	FIV opioi
40	436.8	37.9	9569	13	ADR44842	FIV-NSE-H
41	436.8	37.9	10472	13	ADR44876	Plasmid p
42	434.8	37.7	2162	2	AAV61994	Human mu-
43	434.6	37.7	1464	10	ADG42250	Mu-opioid
44	433.2	37.5	1200	13	ADR44830	Human HUM
45	433.2	37.5	1200	13	ADR44837	HUMOR mut

ALIGNMENTS

```
RESULT 1
ADN30508
ID   ADN30508 standard; cDNA; 1154 BP.
XX
AC   ADN30508;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C1008T allele.
XX
KW   Human; kappa opioid receptor; hKOR; SS; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity,; mood; affect; immune function;
KW   gastrointestinal function; analgesia; addictive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   allele         replace(1008,C)
FT                  /*tag= a
FT                  /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE//) KREEK M J.
PA   (YUFE//) YUFEROV V.
PA   (LAFO//) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
```

PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 4; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR), sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect; immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutic effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C1008T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1154;   DB 12;   Length 1154;
Best Local Similarity   100.0%;   Pred. No. 9.5e-275;
Matches 1154;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGAGCCGGGCCTACCTGCCCGCCCGAGCGCC 60
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Db     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGAGCCGGGCCTACCTGCCCGCCCGAGCGCC 60

Qy    61 TGCCTGCCCCCAAACAGCAGCGCCTGGTTTCCCGGTCGGCCGAGCCCGACAGCAGCACGGC 120
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Qy   121 AGGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCGCCGCACATCTCCCCGGGCATCCCGGTC 180
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Db   121 AGGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCGCGCCGCACATCTCCCCGGGCATCCCGGTC 180

Qy   181 ATCATCACGCGGGGTCTCACTCCGTAGTGTTCGTCGTGGCTTGGTCGTGGGCCAACTCGCTGGTC 240
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Db   181 ATCATCACGCGGGGTCTCACTCCGTAGTGTTCGTCGTGGCTTGGTCGTGGGCCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCACAACATTTACATATTTAAC 300
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Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
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Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGGACCGGTACATTGCCGTG 480
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Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGGACCGGTACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTGCTCCCAGATGATGACTACTCC 660
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Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCAGTTGCTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
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Db   661 TGGTGGGACCTCTTCATGAAGATCTGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGTCCGGCTCCTTTCT 780
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Db   721 ATCATCATGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
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Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 900
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Db   841 GCAGTCTTCGTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 900

Qy   901 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
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Db   901 AGCACCTCCACAGCACAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAATTTCAAGCGGTGT 1020
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Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
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Db  1141 TGACTAGTCGTGGA 1154
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RESULT 2
ADN30505
ID   ADN30505 standard; cDNA; 1154 BP.
XX
AC   ADN30505;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, wild-type cDNA.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol'; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   replace(36,T)
FT   /*tag= a

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Matches 1153;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

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Qy     61 TGCCTGCCCCCAACAGCAGGCGGCCTGGTTCCCGGCTGGGCGGAGCCGGACAGCAACGGC 120
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Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTCGGTC 240
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Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACATTACATATTTAAC 300
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Qy    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db    301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
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Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGCGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACGCGTACATGCCGTG 480
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Db    721 ATCATCGTCTGCTACCACCCTGATGATCCTGGTCTCCAAGAGCGTCCGGCGTCCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGGCTAGGATCACAGTGGTCTGGTGGTG 840
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Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGGCTAGGATCACAGTGGTCTGGTGGTG 840

Qy    841 GCAGTCTTCGTCGTCGTCGTGCTGCAAGATCGCAACTCACATATTCACATATTCACCTGGGG 900
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Qy    901 AGCACCTTCCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTAGGCTAT 960
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Db    901 AGCACCTTCCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTAGGCTAT 960

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Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGCGGCCGCAGCGAGAGTC 1080
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PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Claim 1; SEQ ID NO 1; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful for
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one addictive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the most common, wild-type allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match   99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 2.4e-274;

RESULT 3
ADR44858
ID   ADR44858 standard; cDNA; 1154 BP.
XX
AC   ADR44858;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human kappa opioid receptor encoding cDNA SEQ ID NO:30.
XX
KW   opioid receptor; nerve cell; analgesic; gene therapy; pain; human;
KW   kappa opioid receptor; chromosome 8; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT   /product= "kappa opioid receptor"
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PN   WO2004073646-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-US004914.
XX
PR   19-FEB-2003; 2003US-0448663P.
XX
PA   (UYRP) UNIV ROCHESTER.
XX
PI   Kyrkanides S, Tallents RH;
XX
DR   WPI; 2004-635472/61.
DR   P-PSDB; ADR44857.
DR   GENBANK; U17298.
XX
PT   New vector for delivering an opioid receptor to a nerve cell comprising a
PT   sequence encoding a mu-opioid receptor and a vector backbone, useful in
PT   preparing a composition for reducing pain.
XX
PS   Disclosure; SEQ ID NO 30; 147pp; English.
XX
CC   The present invention describes a vector for delivering an opioid
CC   receptor to a nerve cell. The method comprises a sequence encoding an
CC   opioid receptor and a vector backbone. Also described: (1) a cell
CC   comprising the vector or its integrated product; (2) an animal comprising
CC   the cell; (3) reducing pain in a subject; (4) producing the vector; (5)
CC   producing the cell; and (6) an animal produced by the process of
CC   administering the vector to the animal. The vector is useful in
CC   activity, and can be used in gene therapy. The vector has analgesic
CC   preparing a composition for reducing pain in a subject. The present
CC   sequence encodes the human kappa opioid receptor, which is used in the
CC   exemplification of the present invention. The human kappa opioid receptor
CC   gene is located on chromosome 8, more specifically to 8q11-12.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match   99.9%; Score 1152.4; DB 13; Length 1154;
Best Local Similarity   99.9%; Pred. No. 2.4e-274;
Matches 1153; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Qy  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGAGCTGGCCCGCGTCGAGCCCACATCTCCCGGTC 180
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Db  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGAGCTGGCCCGCGTCGAGCCCACATCTCCCGGTC 180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCCTGGTGGGCAACTCGCTGGTC 240
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Db  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCCTGGTGGGCAACTCGCTGGTC 240

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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Qy  361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTCAAGATAGTAATTCCATTGATTACTAC 420
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Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCTGGACCGCTACATTGCCGTG 480

Qy  481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATAATC 540
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Qy  541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTGTGGCATCTGTGGAGGCACCAAA 600
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Qy  661 TGGTGGGACCTCTTCATGAAGATCGTGCGTCTTCATCTTTGCTTCGTCTTTGCTTTCCTGTCCTC 720
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Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780

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Db  841 GCAGTTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGTGGAGGCTCTCGGGG 900

Qy  901 AGCACCTCCACAGCACAGTCTGCTCTCCAGCTATTACTTCTGCATCGCCTATCGGCCTTAGGCTAT 960
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Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGAATGAGGATGGAGCGGCAGCAGCACTAGCAGAGTC 1080
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Db 1141 TGACTAGTCGTGGA 1154

Qy    1 ATGGACTCCCGATCCAGATCTTCCGGGGAGGAGCCGGGCCTCACCTGCCCCCGAGCGCC 60
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Qy    1141 TGACTAGTCGTTGGA 1154
           ||||||||||||||||
Db    1141 TGACTAGTCGTTGGA 1154

RESULT 4
ADN30506
ID   ADN30506 standard; cDNA; 1154 BP.
XX
AC   ADN30506;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C852T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   allele         replace(852,C)
FT                  /*tag= a
FT                  /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 2; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to the
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance,
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C852T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match             99.7%;  Score 1150.8;  DB 12;  Length 1154;
Best Local Similarity   99.8%;  Pred. No. 5.9e-274;
Matches 1152;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCGGGCCTACCTGCCCCGAGCGCGCC   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCGGGCCTACCTGCCCCGAGCGCGCC   60

Qy    61 TGCCTGCCCCCAACAGCAGCCGGCTGGTTCCGGCCGGAGCCGAGCAGCAGCAACGGC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCCGGCTGGTTCCGGCCGGAGCCGAGCAGCAGCAACGGC  120

Qy   121 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCCGCGCACATCTCCCCGGCCATCCCGGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCCGCGCACATCTCCCCGGCCATCCCGGTC  180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240

Qy   241 ATGTTCGTGATCATCCGATACACAACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAACAAAGATGAAGACAGCAACCAACATTACATATTTAAC  300

Qy   301 CTGGCTTTGGCGAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCGAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG  480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy   541 TGCATCTGGCTGCTGTGTCATCGTGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTGTCATCGTGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA  600

Qy   601 GTCAGGGAAGACGTTGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGACTACTCC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTTGATGTCATTGAGTGTCATTGAGTGTCCCAGATGATGACTACTCC  660

Qy   661 TGGTGGGACCCTTCATGAAGATCGCGTCTTCATCTTTGCCTTGTCGTGATCCCTGTCCTC  720
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Db   661 TGGTGGGACCCTTCATGAAGATCGCGTCTTCATCTTTGCCTTGTCGTGATCCCTGTCCTC  720

Qy   721 ATCATCATCGTCTGCTACACCCTGCTCTGCGATCCTGCGTCTCAAGAGCGTCCGGCTTTCT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACCCTGCTCTGCGATCCTGCGTCTCAAGAGCGTCCGGCTTTCT  780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
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Qy   841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCATCCTGGTGAGGCTCTGGGG   900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTTGTCGCTGGACTCCCATTCACATATTCATCCTGGTGAGGCTCTGGGG   900

Qy   901 AGCACCTCCCACAGCACCAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT   960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCACCAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT   960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT  1020
         |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT  1020

Qy  1021 TTCCGGGACTCTGCTTTCCACTGAAGATGAGGACGGCAGAGCACTAGCAGAGTC      1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGACGGCAGAGCACTAGCAGAGTC     1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy  1141 TGACTAGTCGTGGA  1154
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Db  1141 TGACTAGTCGTGGA  1154
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RESULT 5
ADN30510
ID ADN30510 standard; cDNA; 1154 BP.
XX
AC ADN30510;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human kappa opioid receptor, hKOR, A843G allele.
XX
KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW single nucleotide polymorphism; endogenous opioid system; nociception;
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW amphetamine; alcohol; tobacco; opiate; withdrawal;
KW neuroendocrine function; reproductive function; prolactin regulation;
KW stress responsivity.; mood; affect; immune function;
KW gastrointestinal function; analgesia; additive disease;
KW chromosome 8q11.2.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT allele   replace(843,A)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN US2004097704-A1.
XX
PD 20-MAY-2004.
XX
PF 13-JUL-2001; 2001US-00904584.
PR 14-JUL-2000; 2000US-0218300P.
XX
PA (KREE/) KREEK M J.
PA (YUFE/) YUFEROV V.
PA (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, Yuferov V, Laforge KS;
XX
DR WPI; 2004-389204/36.
XX
PT Novel isolated variant allele of human kappa opioid receptor gene, useful
PT for determining susceptibility in subject to physiological response,
PT condition or disease related to endogenous opioid system.
XX
PS Example; SEQ ID NO 6; 29pp; English.
XX

CC The invention relates to an isolated variant allele of a human kappa
CC opioid receptor gene, comprising a DNA sequence having at least one
CC variation in a fully defined wild-type allele of human kappa opioid
CC receptor (hKOR) sequence appearing as ADN30505, where the variation
CC comprises C852T, C948T, C1008T or their combinations. Also included are
CC an isolated nucleic acid molecule selectively hybridising to the variant,
CC a cloning vector comprising the variant and an origin of replication, an
CC expression vector comprising the variant associated with a promoter, a
CC unicellular host transformed/transfected with the vector and a commercial
CC test kit for determining the presence of at least one variation in a hKOR
CC gene of an allele in a bodily sample taken from a subject. The hKOR
CC variant allele is useful for determining a susceptibility in a subject to
CC at least one physiological response, condition or disease related to the
CC endogenous opioid system, nociception, neurotransmitter release
CC endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC amphetamine and other stimulants self-administration, behavioural
CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC neuroendocrine function, reproductive function, prolactin regulation,
CC stress responsivity, physiology and pathology of mood and affect, immune
CC function, gastrointestinal function. The hKOR variant allele is useful for
CC determining a susceptibility to pain in a subject and is useful for
CC determining a therapeutically effective amount of pain reliever to
CC administer to a subject in order to induce analgesia in the subject. The
CC hKOR variant allele is useful for determining a therapeutically effective
CC amount of therapeutic agent to administer to a subject suffering from at
CC least one addictive disease to treat the at least one additive disease.
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC is theA843G allele of hKOR.
XX
SQ Sequence 1154 BP; 238 A; 339 C; 288 G; 289 T; 0 U; 0 Other;

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity 99.8%; Pred. No. 5.9e-274;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCCGCCCCAGAGCGCC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCCGCCCCAGAGCGCC    60

Qy    61 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGGCTGGGCGGCGAGCCGACAGCAGCAACGGC   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCAACAGCAGCGCCTGGTTCCCGGCTGGGCGGCGAGCCGACAGCAGCAACGGC   120

Qy   121 AGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCGACCATCTCCCGGCCATCCCGGTC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCGACCATCTCCCGGCCATCCCGGTC   180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTTGGTGGGCAACTCGCTGGTC   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCGTTGGTGGGCAACTCGCTGGTC   240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACATGCCCTTTCAGAGTACGGTCTACTTG   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACATGCCCTTTCAGAGTACGGTCTACTTG   300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGGTGTGCAAGATAGTAATTTCCATTGATTACTAC   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGGTGTGCAAGATAGTAATTTCCATTGATTACTAC   420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG   480
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG   480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC   540

Qy   541 TGCATCGGCTGGTCGTGTCGTCATCGTTGGCATCCTGTTGGCAATAGTCTTGAGGCACCAAA   600
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XX
PF     13-JUL-2001; 2001US-00904584.
XX
PR     14-JUL-2000; 2000US-0218300P.
XX
PA     (KREE/) KREEK M J.
PA     (YUFE/) YUFEROV V.
PA     (LAFO/) LAFORGE K S.
XX
PI     Kreek MJ, Yuferov V, Laforge KS;
XX
DR     WPI; 2004-389204/36.
XX
PT     Novel isolated variant allele of human kappa opioid receptor gene, useful
PT     for determining susceptibility in subject to physiological response,
PT     condition or disease related to endogenous opioid system.
XX
PS     Example; SEQ ID NO 3; 29pp; English.
XX
CC     The invention relates to an isolated variant allele of a human kappa
CC     opioid receptor gene, comprising a DNA sequence having at least one
CC     variation in a fully defined wild-type allele of human kappa opioid
CC     receptor (hKOR) sequence appearing as ADN30505, where the variation
CC     comprises C852T, C948T, C1008T or their combinations. Also included are
CC     an isolated nucleic acid molecule selectively hybridising to the variant,
CC     a cloning vector comprising the variant and an origin of replication, an
CC     expression vector comprising the variant associated with a promoter, a
CC     unicellular host transformed/transfected with the vector and a commercial
CC     test kit for determining the presence of at least one variation in a hKOR
CC     gene of an allele in a bodily sample taken from a subject. The hKOR
CC     variant allele is useful for determining a susceptibility in a subject to
CC     at least one physiological response, condition or disease related to the
CC     endogenous opioid system, nociception, neurotransmitter release
CC     endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC     amphetamine and other stimulants self-administration, behavioural
CC     sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC     amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC     neuroendocrine function, reproductive function, prolactin regulation,
CC     stress responsivity, physiology and pathology of mood and affect, immune
CC     function, gastrointestinal function. The hKOR variant allele is useful
CC     for determining a susceptibility to pain in a subject and is useful for
CC     determining a therapeutically effective amount of pain reliever to
CC     administer to a subject in order to induce analgesia in the subject. The
CC     hKOR variant allele is useful for determining a therapeutically effective
CC     amount of therapeutic agent to administer to a subject suffering from at
CC     least one addictive disease to treat the at least one additive disease.
CC     The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC     is the C948T allele of hKOR.
XX
SQ     Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match             99.7%;  Score 1150.8;  DB 12;  Length 1154;
Best Local Similarity   99.8%;  Pred. No. 5.9e-274;
Matches 1152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGGCCCCGAGCGCC 60
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Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGCCCTACCTGCGGCCCCGAGCGCC 60

Qy     61 TGGCTGCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGGGGCCGGCAGCAGGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGCTGCCCCAACAGCAGCGGCCTGGTTTCCCGGCCGGGGCCGGCAGCAGGCAACGGC 120

Qy    121 AGCGCCGGCTCGGAGGACGCGAGCTGAGCCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGCCGGCTCGGAGGACGCGAGCTGAGCCTGGAGCCCGCGCACATCTCCCGGCCATCCGGTC 180

Qy    181 ATCATCACGGCGGTCTACTTCCGTAGTGTTCGTCGTGGCTTGGTGGGGCAACTCGGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTTCCGTAGTGTTCGTCGTGGCTTGGTGGGGCAACTCGGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATCACAAAGATGAAGACAGCAACCAACATTACATATTTAAC 300
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Db    541 TGCATCTGGCTGCTGCGTCGTCATCTGTTGTTGCAATAGTCCTTGGAGGAGGCACCAAA 600
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Qy    601 GTCAGGGAAGAGACGTCGATGTCATTGAGTGCTCCTTCCCAGATGATGACTACTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGAGACGTCGATGTCATTGAGTGCTCCTTCCCAGATGATGACTACTCC 660
Qy    661 TGGTGGGGACCCTGCTTCATGAAGATCTGCGTCTTCATCTTGCCTTGCGTGATCCCTGTCCTC 720
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Db    661 TGGTGGGGACCCTGCTTCATGAAGATCTGCGTCTTCATCTTGCCTTGCGTGATCCCTGTCCTC 720
Qy    721 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCCTCCTTTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCCTCCTTTCT 780
Qy    781 GGTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
Qy    841 GCAGTCTTCGTCGTCTGCTGGGACTCCCATTCACATATTCATCCTGGGTGGAGGCTCTGGGG 900
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Db    841 GCGGTCTTCGTCGTCTGCTGGGACTCCCATTCACATATTCATCCTGGGTGGAGGCTCTGGGG 900
Qy    901 AGCACCTCCACAGCACAGCTGCTCTCTTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCACAGCACAGCTGCTCTCTTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTGGATGAAAATTTCAAGCCGGTGT 1020
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Db    961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTGGATGAAAACTTCAAGCCGGTGT 1020
Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGCGGCAGAGCCACTAGCAGAGTC 1080
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Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGGCGGCAGAGCCACTAGCAGAGTC 1080
Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGGAATGAATAAACCAGTA 1140
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Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGGAATGAATAAACCAGTA 1140
Qy   1141 TGACTAGTCGTGGA 1154
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Db   1141 TGACTAGTCGTGGA 1154
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RESULT 6
ADN30507
ID     ADN30507 standard; cDNA; 1154 BP.
XX
AC     ADN30507;
XX
DT     12-AUG-2004 (first entry)
XX
DE     Human kappa opioid receptor, hKOR, C948T allele.
XX
KW     Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW     single nucleotide polymorphism; endogenous opioid system; nociception;
KW     neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW     amphetamine; alcohol; tobacco; opiate; withdrawal;
KW     neuroendocrine function; reproductive function; prolactin regulation;
KW     stress responsivity.; mood; affect; immune function;
KW     gastrointestinal function; analgesia; additive disease;
KW     chromosome 8q11.2.
XX
OS     Homo sapiens.
XX
FH          Location/Qualifiers
FT     allele     replace(948,C)
FT               /tag= a
FT               /standard_name= "Single nucleotide polymorphism"
XX
PN     US2004097704-A1.
XX
PD     20-MAY-2004.
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Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300

Qy   301 CTGGCTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db   301 CTGGCTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCGTCATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCGTCATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGAGTCGATGGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGAGTCGATGGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 840

Qy   841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGAGGCTCGGGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCACATATTCACATATTCATCCTGGTGGAGGCTCGGGG 900

Qy   901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCCGCCTTAGGCTAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy  1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGACATCGATGGGAGCACTAGCAGAGTC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGACATCGATGGGAGCACTAGCAGAGTC 1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy  1141 TGACTAGTCGTGGA 1154
         ||||||||||||||
Db  1141 TGACTAGTCGTGGA 1154
```

RESULT 7
ADN30511
ID   ADN30511 standard; cDNA; 1154 BP.
XX
AC   ADN30511;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human kappa opioid receptor, hKOR, C855T allele.
XX

CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation,
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one additive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the C846T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match   99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity 99.8%; Pred. No. 5.9e-274;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGA 1154
          |||||||||||||
Db   1141 TGACTAGTCGTGA 1154
```

RESULT 8
ADN30509
ID   ADN30509 standard; cDNA; 1154 BP.
XX
AC   ADN30509;
XX
DT   12-AUG-2004   (first entry)
XX
DE   Human kappa opioid receptor, hKOR, G36T allele.
XX
KW   Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW   single nucleotide polymorphism; endogenous opioid system; nociception;
KW   neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW   amphetamine; alcohol; tobacco; opiate; withdrawal;
KW   neuroendocrine function; reproductive function; prolactin regulation;
KW   stress responsivity.; mood; affect; immune function;
KW   gastrointestinal function; analgesia; additive disease;
KW   chromosome 8q11.2.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   allele   replace(36,G)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2004097704-A1.
XX
PD   20-MAY-2004.
XX
PF   13-JUL-2001; 2001US-00904584.
XX
PR   14-JUL-2000; 2000US-0218300P.
XX
PA   (KREE/) KREEK M J.
PA   (YUFE/) YUFEROV V.
PA   (LAFO/) LAFORGE K S.
XX
PI   Kreek MJ, Yuferov V, Laforge KS;
XX
DR   WPI; 2004-389204/36.
XX
PT   Novel isolated variant allele of human kappa opioid receptor gene, useful
PT   for determining susceptibility in subject to physiological response,
PT   condition or disease related to endogenous opioid system.
XX
PS   Example; SEQ ID NO 5; 29pp; English.
XX
CC   The invention relates to an isolated variant allele of a human kappa
CC   opioid receptor gene, comprising a DNA sequence having at least one
CC   variation in a fully defined wild-type allele of human kappa opioid
CC   receptor (hKOR) sequence appearing as ADN30505, where the variation
CC   comprises C852T, C948T, C1008T or their combinations. Also included are
CC   an isolated nucleic acid molecule selectively hybridising to the variant,
CC   a cloning vector comprising the variant and an origin of replication, an
CC   expression vector comprising the variant associated with a promoter, a
CC   unicellular host transformed/transfected with the vector and a commercial
CC   test kit for determining the presence of at least one variation in a hKOR
CC   gene of an allele in a bodily sample taken from a subject. The hKOR
CC   variant allele is useful for determining a susceptibility in a subject to
CC   at least one physiological response, condition or disease related to the
CC   endogenous opioid system, nociception, neurotransmitter release
CC   endogenous opioid system, learning, memory, cognition, pain, cocaine,
CC   amphetamine and other stimulants self-administration, behavioural
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Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCTACCTGCGCCCGAGCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCTACCTGCGCCCGAGCGCC 60

Qy  61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTCCCGGCCGAGCCGACAGCAACGGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTCCCGGCCGAGCCGACAGCAACGGC 120

Qy 121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCGCGACATCTCCCGGCCATCCCGGTC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGTC 180

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGTGTTCGTGGTGGGCTTGTGGTGGGGGCTTGTGTTCGTGGTGGGCTTGTGGTGGGGCAACTCGCTCGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGTGTTCGTGGTGGGCAACTCGCTCGTC 240

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACACATTTACATATTTAAC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACACATTTACATATTTAAC 300

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTACATTGCCGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTACATTGCCGTG 480

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTCGTCGTGATGTCCATCGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TGCATCTGGCTGCTCGTCGTGATGTCCATCGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy 661 TGGTGGGACCCTCTTCATGAAGATCTGCGGTCTTGCGCTTCGTGATCCCTGTCCTC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 TGGTGGGACCCTCTTCATGAAGATCTGCGGTCTTGCGCTTCGTGATCCCGTCCTCTC 720

Qy 721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy 781 GGCTCCCCAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACCTGGTCCTGGTCGTGGTGGTG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 GGCTCCCCAGAGAAAGATCGCAACCTGCGTAGGATCACCAGATCGCAACCTGCGTAGGATCACCAGACCTGGTCCTGGTCGTGGTGGTG 840

Qy 841 GCAGTCTTCGTCGTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GCAGTTTTCGTCGTGCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACCTCCACCAGACACAGCCCCAGCAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 AGCACCTCCACCAGCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy 961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 ACCAACAGTAGCCTGAATCCCATTCCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGCGAGAGCCACTAGCAGAGTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGCGAGAGCCACTAGCAGAGTC 1080
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CC   sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC   amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC   neuroendocrine function, reproductive function, prolactin regulation;
CC   stress responsivity, physiology and pathology of mood and affect, immune
CC   function, gastrointestinal function. The hKOR variant allele is useful
CC   for determining a susceptibility to pain in a subject and is useful for
CC   determining a therapeutically effective amount of pain reliever to
CC   administer to a subject in order to induce analgesia in the subject. The
CC   hKOR variant allele is useful for determining a therapeutically effective
CC   amount of therapeutic agent to administer to a subject suffering from at
CC   least one addictive disease to treat the at least one addictive disease.
CC   The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC   is the G36T allele of hKOR.
XX
SQ   Sequence 1154 BP; 239 A; 339 C; 286 G; 290 T; 0 U; 0 Other;

Query Match             99.7%;  Score 1150.8;  DB 12;  Length 1154;
Best Local Similarity   99.8%;  Pred. No. 5.9e-274;
Matches 1152;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCGCCCCAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCGCCCCAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120

Qy    121 AGGCGCGGCTCGGAGGACGGCCAGCTGGACGCGGCCGGCCGCCCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGCGCGGCTCGGAGGACGGCCAGCTGGACGCGGCCGGCCGCCCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTGGGCAACTCGCTCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGTGGGCAACTCGCTCGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGAAGATGAACATTTACATATTTAAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGAAGATGAACATTTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCGCCCTTTCAGAGTACGGTCTACTTG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCGCCCTTTCAGAGTACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGCAAGATAGTAATTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTGGGGATGTGCTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTGTCGTCGTCATCGTGTGCATCTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTGTCGTCGTCATCGTGTGCATCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGGATCCCTGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGGATCCCTGTCCTC 720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCGGTCTCAAGAGCGTCCGGCTCCTTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCGGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGGTG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGGTG 840

Qy    841 GCAGTCTTCGTCGTCGTGCTGGACTCCCATTCACATATTCATCCTGGTGTGCGGAGGCCTTCGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCAGTCTTCGTCGTCGTGCTGGACTCCCATTCACATATTCATCCTGGTGTGCGGAGGCCTTCGGG 900

Qy    901 AGCAGCTCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCAGCTCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTGATGAAAATTTCAAGCGGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTGATGAAAACTTCAAGCGGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCGTTCCACTGAAGATGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCGTTCCACTGAAGATGAGGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154


RESULT 9
AB242678
ID   AB242678 standard; DNA; 1182 BP.
XX
AC   AB242678;
XX
DT   04-MAR-2003 (first entry)
XX
DE   Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC, Roush CL, Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81832.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
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XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related diseases, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match             99.2%;  Score 1144.4;  DB 8;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 2.3e-272;
Matches 1148;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGACTCCCCATCCCAGATCTTCCGCGGGGGAGCCGGGCCCTACCTGCCCCCGAGCGCC 60
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGGAATCCCGATTCAGATCTTCCGCGGGGGAGCCGGGCCCTACCTGCCCCCGAGCGCC 73

Qy         61 TGCCTGCCCCCAACAGCAGCGGCGGCGGCGGCTGGTTTCCCGGCTGGGCCGAGCAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 TGCCTGCCCCCAACAGCAGCGGCGGCGGCGGCTGGTTTCCCGGCTGGGCCGAGCAGCAACGGC 133

Qy        121 AGGCGCCGGCTCGGAGGACGCGCAGCTGAGCGCCGGCACATCCCCCGGCCATCCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 AGGCGCCGGCTCGGAGGACGCGCAGCTGAGCGCCGGCACATCCCCCGGCCATCCCCGGTC 193

Qy        181 ATCATCACGGCGGCTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 ATCATCACGGCGGCTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy        241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy        421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 493

Qy        481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy        541 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 TGCATCTGGCTGCTGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy        601 GTCAGGGAAGAGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GTCAGGGAAGAGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy        661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 733

Qy        721 ATCATCATCGTCTGCTACACACCCTGATGATCCTCCGGCTCAAGAGCGTCCGGCTCCTTTCT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 ATCATCATCGTCTGCTACACACCCTGATGATCCTCCGGCTCAAGAGCGTCCGGCTCCTTTCT 793

Qy        781 GGCTCCCGAGAGAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGTGGTGGTGGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 GGCTCCCGAGAGAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGTGGTGGTGGTG 853

Qy        841 GCAGTCTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGAGGCTTCTGGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 GCGGTTTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGAGGCTTCTGGGG 913

Qy        901 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy        961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAATTTCAAGGGGTGT 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAAACTTCAAGGGGTGT 1033

Qy       1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGGAGCGGCAGCACTAGCAGAGTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGGAGCGGCAGCACTAGCAGAGTC 1093

Qy       1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy       1141 TGACTAGTCGTGGA 1154
              ||||||||||||||
Db       1154 TGACTAGTCGTGGA 1167
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RESULT 10
AAD58490

```
ID   AAD58490 standard; DNA; 1182 BP.
XX
AC   AAD58490;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human kappa opioid receptor 1 (KOR) DNA.
XX
KW   Human; urological disorder; urinary incontinence; gene therapy; cancer;
KW   kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
KW   urethra; overflow urinary incontinence; stress urinary incontinence;
KW   nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
KW   kappa opioid receptor 1; KOR; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             14..1156
FT                   /tag= a
FT                   /product= "Human kappa opioid receptor 1 (KOR)"
FT                   /note="The CDS is referred to as SEQ ID NO:21 in the
FT                   specification"
XX
PN   WO2003061573-A2.
XX
PD   31-JUL-2003.
XX
PF   16-JAN-2003; 2003WO-US001450.
XX
PR   18-JAN-2002; 2002US-0349511P.
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PR   28-FEB-2002;  2002US-0360500P.
PR   15-MAR-2002;  2002US-0365041P.
PR   19-APR-2002;  2002US-0374063P.
PR   14-AUG-2002;  2002US-0403468P.
PR   27-SEP-2002;  2002US-0411426P.
PR   21-OCT-2002;  2002US-0419986P.
PR   05-NOV-2002;  2002US-0423809P.
PR   26-NOV-2002;  2002US-0429797P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Silos-Santiago I, Karicheti V;
XX
DR   WPI; 2003-598705/56.
DR   P-PSDB; AAE38589.
XX
PT   Identifying a compound for treating urological disorders, for example
PT   urinary incontinence by assaying the ability of the compound to modulate
PT   the nucleic acid expression or polypeptide activity.
XX
PS   Disclosure; Page 149-151; Opp; English.
XX
CC   The present relates to a method for identifying a compound for treating
CC   urological disorders e.g., urinary incontinence including overactive/
CC   oversensitive bladder, overflow urinary incontinence, stress urinary
CC   incontinence caused by dysfunction of the bladder, urethra or central or
CC   peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC   cancer of the prostate or kidney disorders. The method is also useful for
CC   modulating hyperplasia in a cell and treating a subject having a
CC   urological disorder. The invention is also used in gene therapy. The
CC   present sequence is human kappa opioid receptor 1 (KOR) DNA
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match       99.2%;  Score 1144.4;  DB 10;  Length 1182;
Best Local Similarity  99.5%;  Pred. No. 2.3e-272;
Matches 1148;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy       1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGAGCCTACCTGCGCCCCGAGCGCC  60
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      14  ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGAGCCTACCTGCGCCCCGAGCGCC  73

Qy      61  TGCCTGCCCCCAACAGCAGCGCGGCCTGGTTTCCGCTGGGGCCGGAGCCCGACAGCAACGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74  TGCCTGCCCCCAACAGCAGCGCGGCCTGGTTTCCGCTGGGGCCGGAGCCCGACAGCAACGGC  133

Qy     121  AGGCGCGGCTCGGAGGACGCGCGGCAGCTGGAGCTCCCCGGCACATCTCCCCGGCCATCCCGGTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134  AGGCGCGGCTCGGAGGACGCGCGGCAGCTGGAGCTCCCCGGCACATCTCCCCGGCCATCCCGGTC  193

Qy     181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCAACTCGCTCGGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCAACTCGCTCGGTC  253

Qy     241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  313

Qy     301  CTGGCCTTTGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314  CTGGCCTTTGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  373

Qy     361  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374  ATGAATTCCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC  433

Qy     421  AACATGTTCACCAGCACATCTTCACCTTGACCGCTACATTGCCGTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||
Db     434  AACATGTTCACCAGCATCTTCACCTTGACCGCTACATTGCCGTG  493

Qy     481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     494  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  553
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Qy     541  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGACCAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     554  TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGACCAAA  613

Qy     601  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     614  GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCAGATGATGACTACTCC  673

Qy     661  TGGTGGGACCTTCATGAGAATCTGCGTCTTCACTTTGCCTTCGTGATCCCGTCCTC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     674  TGGTGGGACCTTCATGAGAATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC  733

Qy     721  ATCATCATCCTGCTACACCCTGATGATCCGGGTCTCAAGAGCGTCGGTCTCCTTTCT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     734  ATCAATCATCCTGCTACACCCTGATGATCCGGGTCTCAAGAGCGTCCCGTCTCCTTTCT  793

Qy     781  GGCTCCCGAGAGAAAGATCCAACCTGGCTAGGATCACCAGACGACTGGTCCTGGTGGTG  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     794  GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACGACTGGTCCTGGTGGTG  853

Qy     841  GCAGTCTTCTGCTGCTGCTGACTCCATTCACATATTCACATATTCATCCTGTGTGGAGGCTCTGGGG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     854  GCGGTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGTGTGGAGGCTCTGGGG  913

Qy     901  AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     914  AGCACCTCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  973

Qy     961  ACCACAGTAGCCTGAATCCATTCTTACGGCCTTTCTTGATGAAAATTTCAAGCGGTGT  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     974  ACCACAGTAGCCTGAATCCATTCTTCTACGGCCTTTCTTGATGAAAACTTCAAGCGGTGT  1033

Qy    1021  TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1034  TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC  1093

Qy    1081  CGAAATACAGTTCAGGATCTCGCTTACCTGAGGGATGCATCGATGGGATGAATAAACCAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094  CGAAATACAGTTCAGGATCTCGCTTACCTGCTTACCTGAGGGGACATCGATGGGATGAATAAACCAGTA  1153

Qy    1141  TGACTAGTCGTGGA  1154
            ||||||||||||||
Db    1154  TGACTAGTCGTGGA  1167
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RESULT 11
ADB84861
ID   ADB84861 standard; DNA; 1182 BP.
XX
AC   ADB84861;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Farnesyl transferase inhibitor modulated leukemia associated gene #80.
XX
KW   ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW   quinolinone; leukemia; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200303038129-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US034784.
XX
PR   30-OCT-2001; 2001US-0338997P.
PR   30-OCT-2001; 2001US-0340081P.
PR   30-OCT-2001; 2001US-0340938P.
PR   30-OCT-2001; 2001US-0341012P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
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XX
PI   Raponi M;
XX
DR   WPI; 2003-513497/48.
XX
PT   Determining whether a patient will respond to treatment with a farnesyl
PT   transferase inhibitor, by analyzing the expression of gene that is
PT   differentially modulated in the presence of the inhibitor.
XX
PS   Disclosure; SEQ ID NO 80; 346pp; English.
XX
CC   The invention relates to a method of determining whether a patient will
CC   respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC   analyzing the expression of gene that is differentially modulated in the
CC   presence of an FTI. The method is useful for determining whether a
CC   patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC   chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC   methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC   patient with leukemia with FTI if the analysis indicates that the patient
CC   will respond. This sequence corresponds to a gene whose expression may be
CC   modulated in the presence of FTI.
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match     99.2%;  Score 1144.4;  DB 10;  Length 1182;
Best Local Similarity  99.5%;  Pred. No. 2.3e-272;
Matches 1148;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy     1 ATGGACTCCCCGATCCAGATCTTCCGCGGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    14 ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCCGGGCCCTACCTGCGCCCCGAGCGCC 73

Qy    61 TGCCTGCCCCCAACAGCAGCGGCTGGTTTCCCGGCGTGGGCCGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 TGCCTGCCCCCAACAGCAGCGGCTGGTTTCCCGGCGTGGGCCGAGCCCGACAGCAACGGC 133

Qy   121 AGGGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGGCCGCACATCTCCCCGGCCATCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGGGCCGGCTCGGAGGACGCGGCAGCTGGAGCCCGGCCGCACATCTCCCCGGCCATCCCGGTC 193

Qy   181 ATCATCACGGCCGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCCGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCACCAACATTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAGCACCAACATTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy   361 ATGAATTCCTGGCCTTTGGGATGTGCTGTCGTGCAAGATAATTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTGGGATGTGCTGTCGTGCAAGATAATTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTCGTGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTCGTGTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCTTGCCAGTTCCCAGATGATGACTACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTTCCTTGCCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720
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Db   674 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   721 ATCATCATGCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCGGCTCTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATGCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCGGCTCTTCT 793

Qy   781 GGCTCCCGAGAGAAGATGCAACCTGCTAGGATCACCAGACTGGTCTCTGGTCGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAGATGCAACCTGCTAGGATCACCAGACTGGTCTCTGGTCGTGGTG 853

Qy   841 GCAGTCTTCGTCGTCTGCTGGACTCCCCATTCACATATTCACATATTCTCGGTGGAGGCTCGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCCGTTTCGTCGTCTGCTGGACTCCCATTCACATATTCACATATTCCTGGTGGAGGCTCGGGG 913

Qy   901 AGACACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy  1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGGAGCGAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGGAGCGAGAGCACTAGCAGAGTC 1093

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy  1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db  1154 TGACTAGTCGTGGA 1167
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RESULT 12
ACA56819
ID   ACA56819 standard; cDNA; 1182 BP.
XX
AC   ACA56819;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1417.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
PF   30-JAN-1998;  98US-00016434.
XX
PR   30-JAN-1998;  98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J, Seilhamer JJ;
XX
DR   WPI; 2003-352189/33.
XX
PT   Combination of polynucleotide probes, useful as array elements in a
PT   microarray for monitoring the expression of a number of target
PT   polynucleotides.
XX
PS   Claim 1; SEQ ID NO 1417; 65pp; English.
XX
CC   The invention relates to a combination which, comprises a number of
```

CC   polynucleotide probes comprising a sequence selected from one of the 1490
CC   sequences mentioned in the specification. The combination is useful as an
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
XX   seqdata.uspto.gov/sequence.html?DocID=0650093B1
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match   99.2%;   Score 1144.4;   DB 10;   Length 1182;
Best Local Similarity   99.5%;   Pred. No. 2.3e-272;
Matches 1148;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCCGGAGCCCTACCTGCGGCCCCGAGCGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGGAGCCGGAGCCCTACCTGCGGCCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCACAGCAGCCGCCTGGTTTCCCGCTGGGCCGGAGCCCGACAGCAACGGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCACAGCAGCAGCCGCCTGGTTTCCCGCTGGGCCGGAGCCCGACAGCAACGGC 133

Qy   121 AGGGCCGGCTCGGAGGACGGCAGCTGGGACGTGGAGCCCGGCCGCCGGGCCATCCCCGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGGGCCGGCTCGGAGGACGGCAGCTGGGACGTGGAGCCCGGCCGCCGGGCCATCCCCGGTC 193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTG 373

Qy   361 ATGAATTCTGGCCTTTTGGGGATGCTGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCTGGCCTTTTGGGGATGCTGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCTGGACGCGTTACATTGCCGTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCTGGACGCGCTACATTGCCGTG 493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTTCCTTGCAGTTCCCAGATGATGACTCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy   661 TGGTGGGACACCTTCATGAAGATCTCGCTCTTCATCTTTGCCTTCGTTCGTGATCCCTCCTC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCTCTTCATGAAGATCTCGCTCTTCATCTTTGCCTTCGTTCGTGATCCCTCCTC 733

Qy   721 ATCATCATCGTCTGCTACTCTGTACACCCTGATGATCCTCAAGAGCGTCTCCAAGAGCGTCCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACTCTGTACACCCTGATGATCCTCAAGAGCGTCTCCAAGAGCGTCCCGCTCCTTTCT 793

Qy   781 GGCTCCCGAGAGAAAGATGCAACTGCTAGGATCACCAGACTGGTCCTTGGTGGTGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 GGCTCCCGAGAGAAAGATGCCAACCTGCGTAGGATCACCAGACTGCACCAGACTGCCTCGGTGTGGTGGTG 853

Qy   841 GCAGTGTCTGTCGTGTGGACTCCCATTCCACATATTCATCCTGGTGGAGGCTGTGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTCTGTGGACTCCCATTCACATATTCATCCTGTGTGGAGGCTCTGGGG 913

Qy   901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 973

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATTGGAGCGGGCAGCGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATTGGAGCGGGCAGCGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
           ||||||||||||||
Db   1154 TGACTAGTCGTGGA 1167

RESULT 13
ADI56615
ID   ADI56615 standard; DNA; 1182 BP.
XX
AC   ADI56615;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human polynucleotide probe #1417.
XX
KW   Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW   effector-like polypeptide; cancer; immunopathology; neuropathology;
KW   drug development; toxicology; carcinogenicity;
KW   signalling pathway polypeptide; adrenal gland; bladder; bone;
KW   bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW   diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW   dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS   Homo sapiens.
XX
PN   US2004010136-A1.
XX
PD   15-JAN-2004.
XX
PF   26-NOV-2002; 2002US-00305720.
XX
PR   30-JAN-1998;   98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J, Seilhamer JJ;
XX
DR   WPI; 2004-090520/09.
XX
PT   New composition comprising polynucleotide probes, useful as array
PT   elements in a microarray for monitoring the expression of target
PT   polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic

PT   fragments.
XX
PS   Claim 6; SEQ ID NO 1417; 73pp; English.
XX
CC   The invention relates to a composition of polynucleotide probes
CC   comprising first polynucleotide probes comprising at least a portion of a
CC   gene encoding a receptor-like polypeptide, second polynucleotide probes
CC   comprising at least a portion of a gene encoding a transducing
CC   polypeptide and third polynucleotide probes comprising at least a portion
CC   of a gene encoding an effector-like polypeptide. The probes of the
CC   composition are useful as array elements in a microarray for monitoring
CC   the expression of target polynucleotides. The microarray is useful in the
CC   diagnosis and treatment of cancer, an immunopathology or a
CC   neuropathology. It can also be used for drug discovery and development,
CC   toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC   Microarrays can also be used for monitoring the progression of diseases
CC   that may be associated with the altered expression of signalling pathway
CC   polypeptides. The composition can also be used to purify a subpopulation
CC   of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC   is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC   the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC   an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC   ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC   epilepsy, Alzheimer's disease or depression. This sequence represents a
CC   human polynucleotide probe of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match   99.2%;   Score 1144.4;   DB 12;   Length 1182;
Best Local Similarity   99.5%;   Pred. No. 2.3e-272;
Matches 1148;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGGACTCCCGATCCCAGATCTTCCGCGGGAGCCGCGGCCCTACCTGGCCCCGAGCGCC 60
          |||| ||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGCCCTGCCCTACCTGCCCCCGAGCGCC 73

Qy   61 TGCCTGCCCCCCAACAGCAGCAGCCGCCTGGTTTCCCGGCGTGGGCCGAGCCGACAGCGGC 120
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCCAACAGCAGCAGCCGCCTGGTTTCCCGGCGTGGGCCGAGCCGACAGCGGC 133

Qy 121 AGCGGCCGGCTCGGAGGACGGCGCAGCTGGAGCGCCGCACATCTCCCCGGCCATCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 134 AGCGGCCGGCTCGGAGGACGGCGCAGCTGGAGCGCCGCACATCTCCCCGGCCATCCCGGTC 193

Qy 181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCAACTCGCTGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTCGTGGCAACTCGCTGGTC 253

Qy 241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAAACATTACATATTTAAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAACAGCAGCAACAACATTACATATTTAAC 313

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAATGCCCTTTCAGATGACCGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATGACCGGTCTACTTG 373

Qy 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 433

Qy 421 AACATGTTCACCGACATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTTGACCGCTACACATTGCCGTG 493

Qy 481 TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 494 TGCCACCCCGTGAAGGCTTTGAAGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy 541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATATCCTTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 554 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy 601 GTCAGGGAAGACGTCGATGTCATTGAGTCATTGAGTGCTCCTTGCAGTTCCTTGCAGTGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 614 GTCAGGGAAGACGTCGATGTCATTGAGTCATTGAGTGCTCCTTGCAGTTCCTTGCAGTGACTACTCC 673

Qy 661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTGCCTTCGTGATCCCGTCCTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 674 TGGTGGGACCTCTTCATGAAGATCGGCGTCTTCATCTTGCCTTCGTGATCCCGTCCTC 733

Qy 721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 734 ATCATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 793

Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTACGGTCGTGGTGG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy 841 GCAGTCTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCCTCGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 854 GCGGTTTTCGTCGTCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGG 913

Qy 901 AGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 914 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 973

Qy 961 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTCTTGATGAAAATTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 974 ACCAACAGTAGCCTGAATCCCATTCTTCTCACGCCTTCTTGATGAAAACTTCAAGCGGTGT 1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGCCAGAGCACTAGCAGAGTC 1093

Qy 1081 CGAAATACAGTTCAGGATCTCGATGGGACATCGATGGGATGAATAAACCAGTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCTCGATGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy 1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db 1154 TGACTAGTCGTGGA 1167

RESULT 14
AAT90998
ID   AAT90998 standard; cDNA; 1143 BP.
XX
AC   AAT90998;
XX
DT   14-APR-1998 (first entry)
XX
DE   Human kappa opioid receptor cDNA.
XX
KW   Selective target cell activation; G protein-coupled receptor; RASSL;
KW   gene therapy; cell proliferation; kappa opioid receptor; human;
KW   transgenic animal; arrhythmia; bone disease; seizure;
KW   vascular contraction; disease model; ss.
XX
OS   Homo sapiens.
XX
PN   WO9735478-A1.
XX
PD   02-OCT-1997.
XX
PF   25-MAR-1997;   97WO-US005334.
XX
PR   26-MAR-1996;   96US-00622348.
XX
PA   (REGC) UNIV CALIFORNIA.
XX
PI   Conklin BR;
XX
DR   WPI; 1997-502739/46.

DR   P-PSDB; AAW30297.
XX
PT   Selective activation of target cell expressing modified G protein coupled
PT   receptor - allows control of cellular proliferation, especially for
PT   amplification of transfected cells in gene therapy.
XX
PS   Example 1; Page 74-76; 117pp; English.
XX
CC   This cDNA sequence comprises the coding region for human kappa opioid
CC   receptor (KOR, see AAW30297), a G protein-coupled receptor implicated in
CC   neurotransmission. A novel method for selectively activating a target
CC   cell (TC) comprises: (i) introducing into the cell a nucleic acid
CC   sequence (I) that expresses a G protein-coupled receptor (A) modified to
CC   be activated superiorly by a synthetic ligand (RASSL); and (ii) exposing
CC   the transfected cell to small synthetic molecules (B) that bind to and
CC   activate (A), inducing the G protein coupled cellular response associated
CC   with receptor activation. (A) has: (a) decreased binding affinity for a
CC   selected natural ligand of the native receptor; (b) binding affinity for
CC   (B); and (c) is activated by binding (B) sufficiently to produce the
CC   required cellular response. Also new are: (1) transgenic cells including
CC   heterologous (I) in the genome; (2) cellular implants comprising a TC
CC   transfected with (I); (3) isolated (I); and (4) transgenic non-human
CC   animals expressing (A). Activation of (A) results, in vitro or in vivo,
CC   in cellular proliferation, or secretion of a cellular product,
CC   particularly a heterologous therapeutic protein encoded by a second
CC   inserted nucleic acid sequence. Particularly it is used to expand the
CC   relatively few cells that are successfully transfected during gene
CC   therapy procedures. Other responses that can be regulated are cell
CC   migration and contraction, or pigment production. In transgenic animals,
CC   expression or stimulation of (A) is designed to develop cardiac
CC   arrhythmia, symptoms of bone disease, seizures, vascular contractions,
CC   dementia, neurodegeneration etc., for use as models of these diseases
CC   (claimed). The transgenic animals are also used for production of
CC   improved food products (e.g. increased calcium content in eggshells or
CC   altered fat/lean ratios) or to control fertility or induce labour. A
CC   RASSL derived from KOR, designated RASSL ORI (see AAW30299), was
CC   generated by mutation of the KOR cDNA sequence
XX
SQ   Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match   98.9%; Score 1141.4; DB 2; Length 1143;
Best Local Similarity   99.9%; Pred. No. 1.2e-271;
Matches 1142;   Conservative   0; Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCGCCCGAGCGCGCC   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCTACCTGCCGCCCGAGCGCGCC   60

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGACGCCGCGGCCGCGGCCGACATCTCCCCGGGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGACGCCGCGGCCGCGGCCGACATCTCCCCGGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGCTTGGTGGGCAACTCGCTGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGCTTGGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATACGGTCTACTTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGTGCAATAGTCCTTGGAGGCACCAAA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGCAGTCATTGAGTGCTCCGTCCTCCGAGTTCCCAGATGACTACTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGCAGTCATTGAGTGCTCCGTCCTCCGAGTTCCCAGATGACTACTCC 660

Qy   661 TGGTGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGCGTCTCGTGATCCCTGTCCTC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTCGCGTCTCGTGATCCCTGTCCTC 720

Qy   721 ATCATCATGTCTGCTACACCCTGATGATCCTGCCGTCTCAAGACGGTCCGGCTCCTTTCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATGTCTGCTACACCCTGATGATCCTGCCGTCTCAAGACGGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCGACAGACTGGTCCTGGTGGTG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCGACAGACTGGTCCTGGTGGTG 840

Qy   841 GCAGTCTTCGTCGTCTGGACTCCATTCACATATTCATCTCGGTGGAGGCTCTGGGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCTGGACTCCATTCACATATTCATCTCGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCACAGCACAGCTGCTCTCTCACGCTATTATTACTTCTGCATCGCCTTAGGCTAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCACAGCACAGCTGCTCTCTCACGCTATTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAAAATTCAAGCGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTCTTGATGAAAATTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTCCACTGAAGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGATGAATAAACCAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGATGATGAATAAACCAGTA 1140

Qy   1141 TGA 1143
           |||
Db   1141 TGA 1143

RESULT 15
AAT12550
ID   AAT12550 standard; cDNA; 1142 BP.
XX
AC   AAT12550;
XX
DT   03-SEP-1996 (first entry)
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DE   Human kappa opioid receptor cDNA.
XX
KW   Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW   neurology; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1142
FT   /*tag= a
FT   /product= "kappa_opioid_receptor"
FT   /note= "incomplete termination codon"
XX

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PN   WO9601898-A1.
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995; 95WO-FR000912.
XX
PR   11-JUL-1994; 94FR-00008531.
XX
PA   (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX
PI   Kieffer B, Simonin F;
XX
DR   WPI; 1996-097628/10.
DR   P-PSDB; AAR88722.
XX
PT   New nucleic acid encoding the human Kappa opioid receptor - useful in
PT   diagnosis and therapy, and for isolating receptor ligands and modulators.
XX
PS   Claim 3; Page 13-15; 30pp; French.
XX
CC   This sequence codes for the human kappa opioid receptor and was obtained
CC   from two overlapping cDNA fragments isolated from a human placental cDNA
CC   library. The fragments were amplified from the library using PCR primers
CC   based on the sequence of human genomic clones which hybridised with a
CC   murine delta receptor cDNA probe. Nucleotide probes derived from the
CC   kappa opioid receptor coding sequence are useful for diagnosis of
CC   neurological, cardio- vascular and psychiatric disorders associated with
CC   opioid receptors
XX
SQ   Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match             98.8%;  Score 1140.4;  DB 2;  Length 1142;
Best Local Similarity   99.9%;  Pred. No. 2.2e-271;
Matches 1141;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy    1 ATGGACTCCCGATCTCAGATCTTCCGCGGGGAGCGGCCCCTACCTGCGCCCCGAGCGCC 60
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Db    1 ATGGACTCCCCGATCCCCAGATCTTCCGCGGGGAGCGGCCCCTACCTGCGCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGTGGGCCGCAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGTGGGCCGCAGCAGCAACGGC 120

Qy  121 AGCGGCCGGCTCGGAGGACGGCGCAGCTGGAGAGCGCAGCGCGGCCGCCATCCCCGGTC 180
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Db  121 AGCGGCCGGCTCGGAGGACGGCGCAGCTGGAGAGCGCAGCGCGGCCGCCATCCCCGGTC 180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTAGTACGGTCTACTTG 360
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Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTAGTACGGTCTACTTG 360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420
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Db  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTAC 420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480
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Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480

Qy  481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db  481 TGCCACCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy  541 TGCATCTGGCTGCTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Db  541 TGCATCTGGCTGCTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660
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Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy  661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTGCCTTCGTGATCCCTGTCCCTC 720
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Db  661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCCTC 720

Qy  721 ATCATCATCGTCTGCTACACACCCTGCGTCTCAAGGACGTCCGGCTCCTTTCT 780
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Db  721 ATCATCATCGTCTGCTACACACCCTGCGTCTCAAGGACGTCCGGCTCCTTTCT 780

Qy  781 GGCTCCCGAGAGAAAGATGCAACCTGCCTAGGATCACCAGACTGGTCCTTGGTGTGGTG 840
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Db  781 GGCTCCCGAGAGAAAGATGCAACCTGCCTAGGATCACCAGACTGGTCCTTGGTGTGGTG 840

Qy  841 GCAGTCTTCGTCGTGCTGCGTCTCTGGACTCCCATTCACATTCATCCTGGTGGAGGCTCTCGGGG 900
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Qy  901 AGCACCTCCCACAGCACAGCTGCTCTCCAGTATTACTTCTGCATCGCCTTAGGCTAT 960
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Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGCGGCGGCAGCGCGCACTAGCAGAGTC 1080
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy 1141 TG 1142
         ||
Db 1141 TG 1142


Search completed: April  6, 2005, 13:53:18
Job time : 703.667 secs
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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        April  6, 2005, 12:28:42 ; Search time 215 Seconds
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Scoring table: IDENTITY_NUC
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Searched:      1202784 seqs, 818138359 residues

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           Pred. No. is the number of results predicted by chance to have a
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           and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result         Query
No.   Score   Match  Length DB  ID                        Description
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1     1144.4  99.2   1182   4   US-09-016-434-1417         Sequence 1417, Ap
2     1141.4  98.9   1143   4   US-09-341-446B-1           Sequence 1, Appli
3     1140.4  98.8   1142   3   US-08-765-743-1            Sequence 1, Appli
4     1136.2  98.5   1284   4   US-09-341-446B-3           Sequence 1, Appli
5     1110.2  97.9   1143   4   US-09-826-509-542          Sequence 542, App
6     999.4   86.6   1275   4   US-09-341-446B-5           Sequence 5, Appli
7     994.6   86.2   1275   4   US-09-341-446B-7           Sequence 7, Appli
8     909.2   78.8   1408   4   US-09-214-904-5            Sequence 5, Appli
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10    909.2   78.8   1410   3   US-08-292-694A-1           Sequence 11, Appl
11    869.6   75.4   1000   3   US-08-147-592A-11          Sequence 11, Appl
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21    433.2   37.5   1610   3   US-08-188-275A-1           Sequence 1, Appli
22    433.2   37.5   2160   3   US-09-351-198-1            Sequence 1, Appli
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26    430.8   37.3   1334   4   US-09-761-962A-3           Sequence 3, Appli
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28    430.8   37.3   1365   4   US-09-761-962A-11          Sequence 11, Appl
29    430.8   37.3   1423   4   US-09-761-962A-1           Sequence 1, Appli
30    430.8   37.3   1610   4   US-09-761-962A-16          Sequence 16, Appl
31    430.8   37.3   1729   4   US-09-761-962A-9           Sequence 9, Appli
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33    430     37.3   1182   4   US-09-826-509-546          Sequence 546, App
34    430     37.3   1203   4   US-09-826-509-544          Sequence 544, App
35    429.2   37.2   2229   4   US-09-214-904-1            Sequence 1, Appli
36    427.6   37.1   1542   4   US-09-761-962A-4           Sequence 4, Appli
37    427.6   37.1   1981   3   US-08-387-707-15           Sequence 15, Appl
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40    421     36.5   1829   3   US-08-387-707-7            Sequence 7, Appli
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42    421     36.5   2218   4   US-09-214-904-3            Sequence 3, Appli
43    421     36.5   2219   4   US-08-432-174A-1           Sequence 1, Appli
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45    421     36.5   2272   3   US-08-292-694A-3           Sequence 3, Appli
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ALIGNMENTS

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RESULT 1
US-09-016-434-1417
; Sequence 1417, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;  APPLICANT:  Janice Au-Young
;  APPLICANT:  Jeffrey J. Seilhamer
;  TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;  TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;  NUMBER OF SEQUENCES:  1490
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;   STREET:  3174 PORTER DRIVE
;   CITY:  PALO ALTO
;   STATE:  CALIFORNIA
;   COUNTRY:  USA
;   ZIP:  94304
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/016,434
;   FILING DATE:  HEREWITH
;   CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;   NAME:  Zeller, Karen J.
;   REGISTRATION NUMBER:  37,071
;   REFERENCE/DOCKET NUMBER:  PA-0002 US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (650) 855-0555
;   TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1417:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH:  1182 base pairs
;    TYPE:  nucleic acid
;    STRANDEDNESS:  single
;    TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;    LIBRARY:  GENBANK
;    CLONE:  9532059
; US-09-016-434-1417

  Query Match             99.2%;  Score 1144.4;  DB 4;  Length 1182;
  Best Local Similarity   99.5%;  Pred. No. 1.7e-283;
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RESULT 1 (continued)

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Matches 1148;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60
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Db    14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   73

Qy    61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACCGGC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACCGGC  133

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGATCATCTCCCGGCCATCTCCCGGTC       180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 AGCGCCGGCTCGGAGGACGCGCAGCTGGATCATCTCCCGGCCATCTCCCGGTG       193

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  253

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  313

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  373

Qy   361 ATGAATTCCTGGCCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC     420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ATGAATTCCTGGCCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC     433

Qy   421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATGCCGTG   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATGCCGTG   493

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCCACACCCTTGAAGGCAAAGATCATCAATATC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCCACACCCTTGAAGGCAAAGATCATCAATATC  553

Qy   541 TGCATCTGGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAA   600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGCATCTGGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAA   613

Qy   601 GTCAGGGAAGAGCGTCGATGTCATTGAGTGTCTCCTTGCAGTTCCCAGATGACTACTCC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GTCAGGGAAGAGCGTCGATGTCATTGAGTGTCTCCTTGCAGTTCCCAGATGACTACTCC  673

Qy   661 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TGGTGGGACCTTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  733

Qy   721 ATCATCATCGTCTGCTACACACCCTGACTCGCTGATGATCCTGCGTCTCAAGAGGCGTCGG  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 ATCATCATCGTCTGCTACACACCCTGACTCGCTGATGATCCTGCGTCTCAAGAGGCGTCGG  793

Qy   781 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCGCACCAGACTGGTCCTGGTGGTG   840
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Db   794 GGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCGCACCAGACTGGTCCTGGTGGTG   853

Qy   841 GCAGTCTTCGTCGTCGTGACTCGGACTCCCATTCATCCTTGGTGAAGGCTCTGGGG   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GCGGTTTCGTCGTCGTGACTCGGACTCCCATTCATCCTTGGTGAAGGCTCTGGGG   913

Qy   901 AGCACCTCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCCGATCGCCTTAGGCTAT  960
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Db   914 AGCACCTCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCCGATCGCCTTAGGCTAT  973

Qy   961 AACAACAGTAGCCTGAATCCCATTTCTTGATGAAAATTTCAAGCGGTGT  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 AACAACAGTAGCCTGAATCCCATTTCTTGATGAAAACTTCAAGCGGGTGT  1033

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC  1093
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Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGCATCGATGGGATGAATAAACCAGTA  1140
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Db  1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGCATCGATGGGATGAATAAACCAGTA  1153

Qy  1141 TGACTAGTCGTGA  1154
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Db  1154 TGACTAGTCGTGA  1167
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RESULT 2

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US-09-341-446B-1
; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-341-446B-1

Query Match             98.9%;  Score 1141.4;  DB 4;  Length 1143;
Best Local Similarity   99.9%;  Pred. No. 9.6e-283;
Matches 1142;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  0;

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Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC   60

Qy    61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACCGGC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACCGGC  120

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCCGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCCGTC  180

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
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Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360

Qy   361 ATGAATTCCTGGCCTTTGGGATGCTGTGCAAGATAGTGTGCAAGATAGTAATTTCCATTGATTACTAC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTGGGATGCTGTGCAAGATAGTGTGCAAGATAGTAATTTCCATTGATTACTAC  420

Qy   421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATGCCGTG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCCTGACCATGATGAGCGTGGACCGCTACATGCCGTG  480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC  540

Qy   541 TGATGGCTCTGTCGTCGTCATCTGTTGGCATCTGCGCCCCTACCTGCGCGCCGAGCGCC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 TGATGGCTCTGTCGTCGTCATCTGTTGGCATCTGCGCCCCTACCTGCGCGCCGAGCGCC  613

Qy   601 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACGGC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTTCCCGGCCCGAGCCCGAGCAGCAACGGC  673
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; APPLICATION NUMBER: FR 94/08531
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00912
; FILING DATE: 07-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: NX 1758-1P US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1142
US-08-765-743-1

Query Match   98.8%; Score 1140.4; DB 3; Length 1142;
Best Local Similarity   99.9%;   Pred. No. 1.7e-282;
Matches 1141;   Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGAGCGGCCCTACCTGGCCCCCAGCGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCCAGATCTTCCGCGGGAGCGGCCCTACCTGGCCCCCAGCGCC 60

Qy    61 TGCCTGCCCCCAACAGCAGCGGCGCCCTGGTTTCCCGGCTGGGCCGAGCAGCAACGGC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGGCGCCCTGGTTTCCCGGCTGGGCCGAGCAGCAACGGC 120

Qy   121 AGCGCCGGCTCGGAGCAGCGCGGACGCTGAGCCCGCACATCTCCCGGCCATCCCGGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGCAGCGCGGACGCTGAGCCCGCACATCTCCCGGCCATCCCGGTC 180

Qy   181 ATCATCACGGCGGTCTACTCCGATACACAAAGATGAAGACAGCAACAACATTTACATATTAAC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGTCTACTCCGATACACAAAGATGAAGACAGCAACAACATTTACATATTAAC 240

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTTACATATTTAAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGACGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGACGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480

Qy   481 TGCCACCCCGTGAAGGCTTTGAAGATCATCAATATC 540
         |||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCTGCGTCATCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGCGTCATCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGAGTTCCCAGAGTGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGAGTTCCCAGAGTGACTACTCC 660
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Qy   541 TGCATCTGGCTGCTGCGTCATCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCTGCGTCATCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGAGTTCCCAGAGTGACTACTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGAGTTCCCAGAGTGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTCTGCCTTCGTGATCCCGTCCTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTCTGCCTTCGTGATCCCGTCCTC 720

Qy   721 ATCATCATCGTCTGCTACACACCCTGCGTCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCGTCTGCTACACACCCTGCGTCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGGTAGGATCACCAGACTGGTCCTGGTGGTGTG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGGTAGGATCACCAGACTGGTCCTGGTGGTGTG 840

Qy   841 GCAGTCTTCGTCGTCGTCTGCTGCTGGACTCCCATTCACATATTCATCCGTGGTGGAGGCTCTGGGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCGTCGTCTGCTGCTGGACTCCCATTCACATATTCATCCGTGGTGGAGGCTCTGGGG 900

Qy   901 AGCAACTCCCACACCAGCAGCTGCTCTCTCCAGCTATTACTTCTCTGCCCTTAGGCTAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCAACTCCCACACCAGCAGCTGCTCTCTCCAGCTATTACTTCTCTGCCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCCATTCCTTCTACGCCTTTCTTGATGAAATTTCAAGCCGGTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCCATTCCTTCTACGCCTTTCTTGATGAAAACTTCAAGCCGGTGT 1020

Qy  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCCGGCAGCACTAGCAGAGTC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCCGGCAGCACTAGCAGAGTC 1080

Qy  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy  1141 TGA 1143
         |||
Db  1141 TGA 1143
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RESULT 3
US-08-765-743-1
; Sequence 1, Application US/08765743
; Patent No. 6146835
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, Brigitte
; APPLICANT: SIMONIN, Frederic
; TITLE OF INVENTION: HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,743
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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Qy    661  TGGTGGGACCTCTTCATGAGAGATCTGCGTCTTCATCTTTGCCTTCGTCATCCCTGTCCTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TGGTGGGACCTCTTCATGAGAGATCTGCGTCTTCATCTTTGCCTTCGTCATCCCTGTCCTC  720

Qy    721  ATCATCGTCTGCTACACCCTGCGTCTGCGGTCTCCTGAGAGCGTCCGGCTCCTTTCT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATCATCGTCTGCTACACCCTGCGTCTGCGGTCTCCTGAGAGCGTCCGGCTCCTTTCT  780

Qy    781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCCTGGTGGTG  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCCTGGTGGTG  840

Qy    841  GCAGTCTTCGTCGTCTGCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCAGTCTTCGTCGTCTGCTGGACTCCCATTCATCCTGGTGGAGGCTCTGGGG  900

Qy    901  AGCACCTCCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCCTTAGGCTAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  AGCACCTCCCACAGCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCCTTAGGCTAT  960

Qy    961  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTCTTGATGAAAATTTCAAGCGGTGT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  ACCAACAGTAGCCTGAATCCCATTCTCTACGCCCTTCTTGATGAAAATTTCAAGCGGTGT  1020

Qy   1021  TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGGACGGCAGAGCACTAGCAGAGTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TTCCGGGACTTCTGCTTCTGCTTTCCACTGAAGATGAGGACGGCAGAGCACTAGCAGAGTC  1080

Qy   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy   1141  TG  1142
           ||
Db   1141  TG  1142
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RESULT 4
US-09-341-446B-3
; Sequence 3, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 3
;   LENGTH: 1284
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified KOR
US-09-341-446B-3

  Query Match      98.5%;  Score 1136.2;  DB 4;  Length 1284;
  Best Local Similarity   99.7%;  Pred. No. 2.2e-281;
  Matches 1138;  Conservative   0;  Mismatches   0;  Indels  3;  Gaps   0;
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Qy      2  TGGACTCCCGATCCAGATCTTCCGGGGAGCCCGGGAGCCCCTACCTGCGCCCCGAGCGCCT  61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113  TCGACTCCCGATCCAGATCTTCCGGGGAGCCCGGGAGCCCCTACCTGCGCCCCGAGCGCCT  172

Qy     62  GCCTGCCCCCAACAGCAGCAGCAGGCGCCTGGTTTCCCGGCTGGCCGGGCCGAGCAGCAACGCA  121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62  GCCTGCCCCCAACAGCAGCAGCAGGCGCCTGGTTTCCCGGCTGGCCGGGCCGAGCAGCAACGCA  121
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```
Qy    173  GCCTGCCCCCAACAGCAGCAGGCGCCTGGTTTCCCGGCTGGCCGGGCCGAGCAGCAACGCA  232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122  GCGGCGGCTCGGAGGACGCGGCAGCTGGAGCTGGAGCGCGGCAGCACTCTCCCGGCCATCCCGGGTCA  181

Qy    233  GCGGCGGCTCGGAGGACGCGGCAGCTGGAGCTGGAGCGCGGCAGCACTCTCCCGGCCATCCCGGGTCA  292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182  TCATCACGGGGTCTACTCCGTAGTGTTCGTGTGGGCTGGTCGGTGGCAACTCGCTGGTCA  241

Qy    293  TCATCACGGGGTCTACTCCGTAGTGTTCGTGTGGGCTGGTCGGTGGCAACTCGCTGGTCA  352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC  301

Qy    353  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC  412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302  TGGCTTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGTAGTACTACTACA  361

Qy    413  TGGCTTTGGCAGATGCTTTAGTTACTACAACACCATGCCCTTTCAGTAGTACTACTACA  472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362  TGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA  421

Qy    473  TGAATTCCTGCCCTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA  532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGT  481

Qy    533  ACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGT  592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGGCAAAGATCATCAATATCT  541

Qy    593  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAGGGCAAAGATCATCAATATCT  652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653  GCATCTGGCTGCGTCGTCGTCATCGTTGGCATCGTTGGCATCGTTGGAGGCACCAAAAG  712

Qy    542  GCATCTGGCTGCGTCGTCGTCATCGTTGGCATCGTTGGCATCGTTGGAGGCACCAAAAG  601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602  TCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  661

Qy    653  TCAGGGAAGAGCGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713  GGTGGGACCTCTTCATGAGAGATCTGCGTCTTCATCTTTGCCTTCGTCATCCCTGTCCTCA  772

Qy    662  GGTGGGACCTCTTCATGAGAGATCTGCGTCTTCATCTTTGCCTTCGTCATCCCTGTCCTCA  721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773  GGTGGGACCTCTTCATGAGAGATCTGCGTCTTCATCTTTGCCTTCGTCATCCCTGTCCTCA  832

Qy    722  TCATCGTCTGCTACACCCTGCGTCTGCGGTCTCCTGAGAGCGTCCGGCTCCTTTCTG  781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833  TCATCGTCTGCTACACCCTGCGTCTGCGGTCTCCTGAGAGCGTCCGGCTCCTTTCTG  892

Qy    782  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTGG  841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTGG  952

Qy    842  CAGTCTTCGTCGTCTGCTGGACTCCCATTCATCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA  901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953  CAGTCTTCGTCGTCTGCTGGACTCCCATTCATCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA  1012

Qy    902  GCACCTCCCACAGCACAGCAGCTGAATCCATTCTCTACGCCTTTCTTGATGAAAATTCAAGCGGTGTT  961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013  GCACCTCCCACAGCACAGCAGCTGAATCCATTCTCTACGCCTTTCTTGATGAAAATTCAAGCGGTGTT  1072

Qy    962  CCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073  CCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGTT  1132

Qy   1022  TCCGGGACTTCTGCTTTCCACTGAAGATGAGGACGGCGGCAGAGCACTAGCAGAGTCC  1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133  TCCGGGACTTCTGCTTTCCACTGAAGATGAGGACGGCGGCAGAGCACTAGCAGAGTCC  1192

Qy   1082  GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAT  1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193  GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAG  1252

Qy   1142  G  1142
           |
Db   1253  G  1253
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```
RESULT 5
US-09-826-509-542
; Sequence 542, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
;   APPLICANT: Lehmann-Bruinsma, Karin
;   APPLICANT: Liaw, Chen W.
;   APPLICANT: Lin, I-Lin
;   TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
;   TITLE OF INVENTION: Protein-Coupled Receptors
;   FILE REFERENCE: AREN-207
;   CURRENT APPLICATION NUMBER: US/09/826,509
;   CURRENT FILING DATE: 2001-04-05
;   PRIOR APPLICATION NUMBER: 60/195,747
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: 09/170,496
;   PRIOR FILING DATE: 1998-10-13
;   NUMBER OF SEQ ID NOS: 589
;   SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 542
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-826-509-542

  Query Match             97.9%;  Score 1130.2;  DB 4;  Length 1143;
  Best Local Similarity   99.3%;  Pred. No. 7.1e-280;
  Matches  1135;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCCCCCGAGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCTGCGCCCTACCTGCGCCCCGAGCGGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTTCCCGGCTGGGCGCCGAGCCCGACAGCAACGGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCGCGCTGGTTTCCCGGCTGGGCGCCGAGCCCGACAGCAACGGC 120

Qy    121 AGCGGCCGGCTCGGAGGACGCGGCAGCTCGAGCTCGAGCCGCGGCCACATCTCCCGGCCATCCCCGGTC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCGGCCGGCTCGGAGGACGCGGCAGCTCGAGCCGCGGCCACATCTCCCGGCCATCCCCGGTC 180

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACCAACATTACATATTTAAC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACAACCAACATTACATATTTAAC 300

Qy    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATGACGGTCTACTTG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGATGACGGTCTACTTG 360

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy    421 AACATGTTCACCAGCATCTTCACCCTTGACCGTGGACCGCTACATTGCCGTG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATGTTCACCAGCATCTTCACCCTTGACCGTGGACCGCTACATTGCCGTG 480

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGCAAGGCAAAGATCATCAATATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGCAAGGCAAAGATCATCAATATC 540

Qy    541 TGCATCTGGCTGCTCTGTCGTCATCTGTTGGGCATCTGGTGGCATCCTCTGCAATAGTCCTTGCAATAGTCCTTGGAGGCACCAAA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATCTGGCTGCTCTGTCGTCATCTGTTGGGCATCTGGTGGCATCCTCTGCAATAGTCCTTGCAATAGTCCTTGGAGGCACCAAA 600

Qy    601 GTCAGGAGAAGACGTCGATGTCATTGATTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGGAGAAGACGTCGATGTCATTGATTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy    661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTCGCCTTGCCTTCGTGTCCTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGGTGGGACCTCTTCATGAAGATCTGCCTCTTCATCTTTGCCTTCGTCGTGTCCTC 720

Qy    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCT 780

Qy    781 GGCTCCCGAGAGAAAGATGCAACCTGCTAGGATCACCAGACTGGTCTCTGGTGTGGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTCCCGAGAGAAAGATGCAACCTGCGTAGGATCAAGAGACTGGTCTCTGGTGTGGTG 840

Qy    841 GCAGTCTCTGCGTCGTGCTGCGGACCCCATTCACAGATTCATCCTGGTGGAGGCTCTGGGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGGTTTTCGTGCTGCTGGACTCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900

Qy    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960

Qy    961 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCCACTCAAGAATGAGGATGAGGCGGCACTAGCAGAGTC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTTCCCACTGAAGAATGAGGATGAGGCGGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGA 1143
            ||
Db   1141 TGA 1143


RESULT 6
US-09-341-446B-5
; Sequence 5, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of a G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RASSL OR1
US-09-341-446B-5

  Query Match             86.6%;  Score 999.4;  DB 4;  Length 1275;
  Best Local Similarity   93.0%;  Pred. No. 2.6e-246;
  Matches  1061;  Conservative    0;  Mismatches   71;  Indels    9;  Gaps    1;

Qy      2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGCGCCCCGAGCGCCT 61
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCCT 172
```

Db   1244 G 1244

RESULT 7
US-09-341-446B-7
; Sequence 7, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
;   APPLICANT: Conklin, Bruce R.
;   TITLE OF INVENTION: Selective Target Cell Activation By
;   TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
;   TITLE OF INVENTION: Superiorly By Synthetic Ligand
;   FILE REFERENCE: UCAL-049CIP
;   CURRENT APPLICATION NUMBER: US/09/341,446B
;   CURRENT FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US97/05334
;   PRIOR FILING DATE: 1997-03-25
;   PRIOR APPLICATION NUMBER: US 08/622,348
;   PRIOR FILING DATE: 1996-03-26
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RASSL OR2
US-09-341-446B-7

Query Match   86.2%;   Score 994.6;   DB 4;   Length 1275;
Best Local Similarity 92.7%;   Pred. No. 4.5e-245;
Matches 1058;   Conservative 0;   Mismatches 74;   Indels 9;   Gaps 1;

Qy   2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCTCACCTGCGCCCCGAGCGCCT 61
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 TCGACTCCCCCATCCAGATCTTCCGCGGGGAGCCGGGCCTCACCTGCGCCCCGAGCGCCT 172

Qy   62 GCCTGCCCCCAAACAGCAGCCCTGGTTTCCGCGTGGGCGTGGGCCGAGCCGACAGCAACGGCA 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 GCCGCCGGCTCGGACGCGGACGCGGACGCCGCGACATCTCCCGGCCGCCGACAGCAACGGCA 232

Qy   122 GCGCCGGCTCGGACGCGGACGCGGACGCCGCGACATCTCCCGGCGGTGGGCTTGGTCGTCGGTCA 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 GCGCCGGCTCGGAGACGCGGACGCGGACGCCGCGACATCTCCCGGCGGTGGGCTTGGTCGTCGGTCA 292

Qy   182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGCTTGGTCGTCGGTGGCTTGGTGGGCAACTCGCTCGTCA 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGCTTGGTGGGCAACTCGCTCGTCA 352

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAACC 301
               ||||||||||||||||||||||||||||||||||||||||||||
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 361
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 472

Qy   362 TGAATTCCTGGCCTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421
               ||||||||||||||||||||||||||||||||||||||||||||||
Db   473 TGAATTCTTGGCCTTTGGGATGTGCTGTGCAAGATGTTCGTGCAAGATTGTCATTTCCATTGACTACTACA 532

Qy   422 ACATGTTCACCAGACATTCACCTTGACCTGGACTTCCGCACACCTTGACCCGTGT 481
               |||||||||||||||||||||||||||||||||||||||||
Db   533 ACATGTTTACCAGACATTCACCTTGACCTGGACCATGATGAGTGTGACCGTGT 592

Qy   482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCT 541
               ||||||||||||||||||||||||||||||||||||||||||||
Db   593 GCCACCCGTGAAAGCTTTGGATTTCGAACACCTTTGAAAGCAAAGATCATCAACATCT 652

Qy   542 GCATCTGGCTGCTGCTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAG 601
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 GCATTTGGCTACTGGCCATCATCGTTGGTATATCAGCGATAGTCCTTGGGGTGACCCAAC 712

Qy (left column continued)

Qy   62 GCCTGCCCCCAAACAGCAGCCCTGGTTTCCGCGTGGGCGTGGGCCGAGCCGACAGCAACGGCA 121
Db   173 GCGCCGGCTCGGACGCGGACGCGGACGCCGCGACATCTCCCGGCCGCCGACAGCAACGGCA 232

Qy   122 GCGCCGGCTCGGACGCGGACGCGGACGCCGCGACATCTCCCGGCGGTGGGCTTGGTCGTCGGTCA 181
Db   233 GCGGCCGGCTCGGAGACGCGGACGCGGACGCCGCGACATCTCCCGGCGGTGGGCTTGGTCGTCGGTCA 352

Qy   182 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGCTTGGTGGGCAACTCGCTCGTCA 241
Db   233 TCATCACGGCGGTCTACTCCGTAGTGTTCGTGCTTGGTGGGCAACTCGCTCGTCA 352

Qy   242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAACC 301
Db   353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAACC 412

Qy   302 TGGCTTTGGCAGATGCTTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 361
Db   413 TGGCTTTGGCAGATGCTTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGA 472

Qy   362 TGAATTCCTGGCCTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421
Db   473 TGAATTCTTGGCCTTTGGGATGTGCTGTGCAAGATGTTCATTTCCATTGACTACTACA 532

Qy   422 ACATGTTCACCAGACATTCACCTTGACCTGGACTTCCGCACACCTTGACCCGTGT 481

Qy   593 GCATCTGGCTGCTGCTCGTCATCGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAG 652

Qy   653 GCATTTGGCTACTGGCCATCATCGTTGGTATATCAGCGATAGTCCTTGGGGTGACCCAAC 712

Db   602 TCAGGGAAGACGTCGATGTCCATTGCATTGAGTGCTCCCAGATGAGTGACTACTCCT 661

Db   713 CCCGGGATGGATGGCAGTGGATGTATGCACGCGCTCCAGTTCCCCCAGCCC------CAGCTGTGT 763

Db   662 GGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCGTGTCCTCA 721

Db   764 ACTGGGACACTGTGACCAAGATCTGGTCTTCATCTTTGCCTTCGTGATCCGTGTCCTCA 823

Db   722 TCATCATCGTCTGCTACACACCCGTAGGATCGATCCTGCGTCCCAGAGCGTCCGGCTCCTTCTG 781

Db   824 TCATCATCGTCTGCTACACCCCGTAGGATCCGTGCGTCCCAGAGCGTCCGGCTCCTTCTG 883

Db   782 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTGG 841

Db   884 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGTGGTGGTGG 943

Db   842 CAGTCTTCGTCGTCTGTCGGACTCCATTCATCCTGCTGACTCCCATTCATCCTGGTGGGGA 901

Db   944 CAGTCTTCGTCGTCTGTCGGACTCCATTCATCCTGCTGACTCCCATTCATCCTGGTGGGGA 1003

Db   902 GCACCTCCCACAGACAGCTGAATCCATTCTTCTCCGCACTACTTCTGCATCGCCTTAGGCTATA 961

Db   1004 GCACCTCCCACAGACAGCTGAATCCATTCTTCTCCGCACTACTTCTGCATCGCCTTAGGCTATA 1063

Db   962 CCAACAGTAGCCTGAATCCATTCTTCTTGATGAAAATTTCAAGCCGGTGTT 1021

Db   1064 CCAACAGTAGCCTGAATCCATTCTTCTTGATGAAAAACTTCAAGCCGGTGTT 1123

Db   1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGAGCAGAGCACTAGACAGTCC 1081

Db   1124 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGAGCAGAGCACTAGACAGTCC 1183

Db   1082 GAAATACAGTTCAGGATCTCAGGAGTTGCTTACCTGAGGAGGACATCGATGGATGAATAAACCAGTAT 1141

Db   1184 GAAATACAGTTCAGGATCTCAGGGAAGCTTACCTGAGGAGGACATCGATGGATGAATAAAACCAGTAG 1243

Qy   1142 G 1142

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;                 LOCATION:  184..1323
US-09-214-904-5

Query Match             78.8%;  Score 909.2;  DB 4;   Length 1408;
Best Local Similarity   86.7%;  Pred. No. 3.7e-223;
Matches 1001;  Conservative    0;  Mismatches 153;  Indels    0;  Gaps    0;
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Qy     1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGAGCCGGGGCCCTACCTGCGCCCCAGCGCGC 60
           |||| || ||| ||||||||||||| || |||| ||| ||||||||||||| | |||||| |
Db   184 ATGGAGTCCCCCATTCAGATCTTCCGAGGAGATCCAGGGCCCTACCTGCTCTCCCAGTGCT 243

Qy    61 TGCCTGCCCCCAACAGCAGCGCGCCTGGTTCCCGCGGTTTCCCGGCGCCTGGGCCGCAACGGC 120
           ||||| |||||||||||||||| |  ||||||| |   |  ||||| ||   |||| ||||| |
Db   244 TGCCTTCTCCCAACAGCAGCAGCTCTTGGTTCCCCAACTGGCAGAATCCGCGGCCATCCCGGGTC 303

Qy   121 AGGCCGGCTCGGAGGACGGCGCAGCTGGAGCTGGAGCTGGCCACATCTCCCGGCCATCCCGGTC 180
           ||  ||| ||||| |||||| ||   |||||| ||| |||||||||||||| |||| |||| || 
Db   304 AGTGTGGGCTCAGAGAGCCAGCAGCGGAGTCGGAGTCGGCCACATCTCCCGGCCATCCCGGTT 363

Qy   181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGAGTGTTGGGTGGGCAACTCGTGGTC 240
           |||||| |  | || |||||| |  || |||||| ||| ||| |||| |||| |||||||| 
Db   364 ATCATCACCGCGTCTACTCTGTGTGTATTTGTGGTGAGTGTTGGGTGGGCAATTCTGGGTC 423

Qy   241 ATGTTCGTGATCATCCGATCACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
           ||||| || || ||||||||||||| |||| |||  ||||||||| ||||| ||| ||| 
Db   424 ATGTTTGTCATCATCCGATCACGAAGATGAAGACCGCAACCAACATCTACATATTAAAC 483

Qy   301 CTGGCTTTGCAGATGCTTAGTTACTACAACCATGCCCTTCAGATGACGGTCGTCTACTTG 360
           |||||||| |||||||| |||||||||||||||||| ||||||||||| || ||||| || 
Db   484 CTGGCTTTGGCAGATGCTTGGTTACTACCACTACCATGTCCTTCAGATGCGTGTCGTCTACTTG 543

Qy   361 ATGAATTCCTGGCCTTTGGGGATGGTGCTGTGCAAGATAGTAATTTCATTGATTACTAC 420
           |||| || ||||| ||||| ||||| || || |||| || ||| || ||||| || ||| 
Db   544 ATGAATTCTTGGGCCTTTGGGAGATGTGCTGTGCAAGATTGTCATTTCCATTGACTACTAC 603

Qy   421 AACATGTTCACCAGCATCTTCACCTTGGACTTCCCGCACCCTGAAGGCAAAGATCATCAATATC 480
           ||||||||| || ||||||||| |||||| ||||| ||||||||||| ||||||||||| ||||
Db   604 AACATGTTTACCAGCATATTCACCTTGGACTTCCCGACCATGAGTGTGGACCGCTACATTGCCGTG 663

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCCGCACTTCCCGCAAGATCCTTGAAGGCACCAAA 540
           |||||||| || |||||||||||| || |||  |||||||||||||   ||| ||||||||
Db   664 TGCCACCCTGTGAAGGCTTTGGACTTGGACTCTGTTGTATATCAGCGGATAGTCCTTGGAGGCACCAAA 723

Qy   541 TGCATCTGCTGTGTCGTCATCTTGTTGGCATCTTCTGCAATAGTCCTTGGAGGCACCACTCC 600
           |||| ||||| |||||| |||||| |||| |||||| ||  | ||| |||||||| || ||| 
Db   724 TGCATTTGCTCCTGGCATCATCTGTTGTGTATATCAGCGGATAGTCCTTGGAGGCACCAAA 783

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT 661
           || |||| ||||| ||||||| |||| || ||||| ||||||||||| |||| |||||| |
Db   784 GTCAGGGAAGATGTGGATGTCATTGAATGCTCCTTGCAGTTTCCTGATGATGATCCTTGTCCCTC 843

Qy   661 ...
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Qy   602 TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT 661
           || |||| ||||| ||||||| |||| || ||||| |||| |||||| |||| |||||| |
Db   713 CCCGGGATGGAGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTCTTCGTGATCCCTGTCCTCA------CAGCTGGT 763

Qy   662 GGTGGGACTTGTCTTCATGAAGATCGCGTCTTCGTCTTTGCCGTCTTCATCTTTGCTCTTCGTGATCCCTGTCCTCA 721
           ||||||||| |||||||||||||||| | ||||| |||||||| ||||||||||| |||||||||||||||||||||
Db   764 ACTGGGACACTGTCTACTACACCCTGATGATCCTGCGGCTCTTTGGCGTCTTCATCTTTGCTCTTCGTGATCCCTGTCCTCA 823

Qy   722 TCATCATCGTCTGCTACACACCCTGATGATCCTGCGGCTCTTCTTCTTGGTCTCTTCTG 781
           |||||||| |||||||||||||| ||||||||||||||||| || || ||||| |||||
Db   824 TCATCATCGTCTGCTACACACCCTGATGATCCTGCGGCTCTTCTTCTTGGTCTCTTCTG 883

Qy   782 GCTCCCGAGAGAAAGATCGCAACCTGCGCAGGATCACCAGACTCGTTGGTCTGGTTGGTGG 841
           ||||||||||| |||| || |||| |||||| |||||||| ||| |||| ||||||||||||
Db   884 GCTCCCGAGAGAAAGATCGCAACCTGCGCAGGATCACCAGACTCGTTGGTCTCCTGGTGTGGTGG 943

Qy   842 CAGTCTTCGTCGTCTGGACTTGCGTTGGACTTCATATTCACATATTCACATATTCAGGGCTCTGGGGA 901
           ||||| ||||| |||||| || | || |||||| ||||||||||||||||  |||||| ||| |||| 
Db   944 CAGTCGTTCGTCGTCTGGACTTCGGACTTCATATTCACATATTCATCTCAGTAGTTCAGGCTCTCGGGGA 1003

Qy   902 GCACCTCCCACAGCACAGCAGCTGCTCTCCCAGCTATTACTTCTGCATCGCTTAGGCTATA 961
           |||| ||||||||||| ||||||| ||||||||||||||||||| || ||  | |||||||
Db  1004 GCACCTCCCACAGCACAGCAGCTGCTCTCCCAGCTATTACTTCTGCATCGCTTAGGCTATA 1063

Qy   962 CCAACAGTAGCCTGAATCCCATTCCTACGCGCCTTCTCTACGCGTCAAGCGGTGTT 1021
           ||||||||| ||||||||||||||| ||  |||||  || ||||| ||||||||||
Db  1064 CCAACAGTAGCCTGAATCCCATTCCCATTCCTCCACTGCTCTACGCGTCAAGCGGTGTT 1123

Qy  1022 TCCGGGACTTCTGTCTTCTGCACTGAAGATGAGGATGGAGGCGGCGGAGAGCACTAGAGAGTCC 1081
           ||||||||| ||||||| ||| ||||||||||| || ||||||| ||||||||||| ||||||
Db  1124 TCCGGGGATCTCTGTCTTCTGCACTGAAGATGAGGATGGAGGCGGCGGAGAGCACTAGCAGTGAGTCC 1183

Qy  1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTAT 1141
           |||||||| ||| |||||||| ||||| || |||||| |||| || ||| ||||||| ||
Db  1184 GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGGATGGAATAAACCAGTAG 1243

Qy  1142 G 1142
         |
Db  1244 G 1244
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RESULT 8
US-09-214-904-5
; Sequence 5, Application US/09214904
; Patent No. 6632977
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION:  TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
;   TITLE OF INVENTION:  OF OPIATE RECEPTORS IS MODIFIED
;   NUMBER OF SEQUENCES:  6
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/214,904
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/FR97/01282
;     FILING DATE:
;     APPLICATION NUMBER:  FR 96.08810
;     FILING DATE:  15-JUL-1996
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1408 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   FEATURE:
;     NAME/KEY:  CDS
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Db   1144 ACCAACAGCAGCCTGAATCCTGTCTCTATGCCTTTCTGGATGAAAACTTCAAGCGGTGT 1203
               |||||||||||| ||||||||||| ||||  | ||||||| |||||
Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAGGATGAGGACGGCGCAGAGCACTAGCAGAGTC 1080

Db   1204 TTTAGGGACTTCTGCTTCCTATTAAGATGCGAATGGAGCGCCAGAGCACCAATAGAGTT 1263
               | |||||||||||||||||  ||||||||  || |  | ||||||||||||
Qy   1081 CGAAATACAGTTCAGGATCCGCTTACCTGAGGGACATCGATGGGAGAATAAACCAGTA 1140

Db   1264 AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGGAGGGATGAATAAGCCAGTA 1323
               ||||| |||||||||||||||| ||| |    ||||||||||||||| |||||
Qy   1141 TGACTAGTCGTGGA 1154
               ||||||||||||||
Db   1324 TGACTAGTCGTGGA 1337


RESULT 9
US-08-147-592A-1

; Sequence 1, Application US/08147592A
; Patent No. 6096513
GENERAL INFORMATION:
  APPLICANT: Bell, Graeme I
  APPLICANT: Reisine, Terry
  APPLICANT: Yasuda, Kazuki
  TITLE OF INVENTION: Opioid Receptor Genes,
  TITLE OF INVENTION: Compositions and Methods
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: Texas
    COUNTRY: United States of America
    ZIP: 72210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/147,592A
    FILING DATE: 05-NOV-1993
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/100,694
    FILING DATE: 30-JUL-1993
    CLASSIFICATION: 435
    APPLICATION NUMBER: 08/066,296
    FILING DATE: 20-MAY-1993
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Wilson, Mark B.
    REGISTRATION NUMBER: 37,259
    REFERENCE/DOCKET NUMBER: ARCD:105
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (512) 418-3000
    TELEFAX: (512) 474-7577
    TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1410 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 186..1325
US-08-147-592A-1
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Qy      1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGGCGGCGCCTCACTGCGCCCCCAGCGCC 60
               ||||||||||||||||| | |||||||||||||||||||||||||||||||
Db    186 ATGGAGTCCCCCATTCAGATCTTCCGAGAGATCAGGCCGCCTACCTGCTCTCCCAGTGCT 245

Qy     61 TGCCTGCCCCCAACAGCAGCGCGTCTTGGTTTCCCGGCTGGGCGGCCGAGCCGACAACGGC 120
               ||||||||||||||||||||||| ||||||||  ||||||||||  ||| ||
Db    246 TGCCTTCTCCCCAACAGCAGCTCTTGGTTCCCCACTGGGCAGAATCCGACAGCAGTAATGGC 305

Qy    121 AGGCGCCGGCTCGGAGGACGCGGCAGCTGGAGCCGGCGCCGGGCCACATCTCCCCGGCCATCCGGTC 180
               ||| |||||||||||||||||||||| |||||||||||||||||||||||
Db    306 AGTGTGGGCTCAGACGGCTCAGCAGCAGCTGGAGCTCCGGGCCACTCGCTGGTC 365

Qy    181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ATCATCACCGCGTGTCTACTCCGTGTGTTCGTGGTGGGCTTAGTGGGCCAATTCTCTGGTC 425

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
               |||||||||||||||||||||||||||||||||||||  ||||| |||||||||||
Db    426 ATGTTTGTCATCATCCGATACACAGAGAGATGAAGACCGCAACCAACATCTACATATTTAAC 485

Qy    301 CTGGCCTTGGCAGATGCTTTAGTTACTACACAACCATGCCCTTCAGATGACGGTCTACTTG 360
               |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    486 CTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTCAGAGTGTTGTCTACTTG 545

Qy    361 ATGAATTCCTGGCCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
               ||||| |||||||||| ||||||||||||||||||||| |  ||||||||||||||
Db    546 ATGAATTCTTGGCCTTTGGAGATGTGCATGCAAGATTGTCATTTCCATTGACTACTAC 605

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGCTACATTGCTGTG 665

Qy    481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCTTCCGACACCTTGAAGCAAAGATCAATATC 540
               |||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db    666 TGCACCCCTGTGAAAGCTTTGGACTTTGGACTTTGAAAGCAAAGATCATCAACATC 725

Qy    541 TGCATCTGGCTGCTCGTCATCGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
               |||||||||||||| | |||| ||||||||  || ||||||||||||||||||||
Db    726 TGCATTTGGCTCCTGGCCATCATCGTGGTATATCAGCGATAGTCCTTGGAGGCACCAAA 785

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTCAGGGAAGATGTGGATGTCATTGAATGCTCGTCCTTGCAGTTCCTGATGATGAATATTCC 845

Qy    661 TGGTGGGACCTCCTTCATGAAGATCGCTGTCTTCATCTTGCCTTCGTGTCCTC 720
               ||| ||||||||||||||||||||||| |||||||||| |||||| || |||||
Db    846 TGGTGGGGATCTCTTCATGAAGATCGTGTGTCTTCGTCTTTGTGATCCCAGTCCTC 905

Qy    721 ATCATCATGTCGTCTGCTGCACCCGATGATCCCGATCTCGCTCGGCTCCGGCTCCTTTCT 780
               |||||||||||||||||||||||||||||||||||| ||  |||||||||||||||
Db    906 ATCATCATTGTCTGCTGCTGCACCCGATCCCGATCTCGCCGCCTGGCTCCGGCTCCTGTCT 965

Qy    781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCGCTAGGATCACCAGGATCCTGGTG 840
               ||||||||||| ||| |||| ||||| |||||||| ||||||||||||||||||||
Db    966 GGCTCCCGAGAGAGAAGGCCGCGAAATCCCGCCGCATCACCAGGATCTGTGCTGTGTAGTAGTT 1025

Qy    841 GCAGTTCCCAGCACACAGCTGACTCCATTCTCATCCTGGTGGGAGCTCTGGGG 900
               |||||||||||||||||||||||||| |||||| |||||| |||||||||||
Db   1026 GCAGTCTTCATCATCTGTTGACCCCCATTCCACCATTCCCAGCTATTACTTCTGGGA 1085

Qy    901 AGCACCTTCCACAGCACAGCTGGTGCCCCTCCCAGCTTAGGCTAT 960
               ||||||||||||||||||||||||||||||| |||||||||||
Db   1086 AGCACCTTCCCACCACCAGCAGCTGCCCCTCCAGCTATTATTTCGTGGGGTTAT 1145

Qy    961 ACCAACAGTAGCTGGACTCCATTCTCTTACGCCTTCTTGATGAAATTTCAAGCCGGTGT 1020
               ||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db   1146 ACCAACAGCAGCCTGGACTTCTGTTTCCATGAGAGATGTGGGATGAATAAACTTCAAGCCGGTGT 1205

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAGGATGAGGACGGCGCAGAGCACTAGCAGAGTC 1080
               ||||||
Db   1206 TTTAGGGACTTCTGCTTCCCTATTAAGATGCGAATGGAGCGCCAGAGCACCAATAGAGTT 1265

Qy   1081 CGAAATACAGTTCAGGATCCGCTTACCTGAGGGACATCGATGGGAGGGATGAATAAACCAGTA 1140
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Query Match     78.8%;  Score 909.2; DB 3;  Length 1410;
Best Local Similarity  86.7%;  Pred. No. 3.7e-223;
Matches 1001;  Mismatches  0;  Conservative  0;  Indels 153;  Gaps  0;
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Db 1266 AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGAGATGTGGGAGGGATGAATAAGCCAGTA 1325
              |||| |||||||||||||||||||||||| |||| || ||||||||| |||||||||||||||
Qy 1141 TGACTAGTCGTGGA 1154
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Db 1326 TGACTAGTCGTGGA 1339
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RESULT 10
US-08-292-694A-1
; Sequence 1, Application US/08292694A
; Patent No. 6319686
; GENERAL INFORMATION:
; APPLICANT: BELL, GRAEME
; APPLICANT: REISINE, TERRY
; APPLICANT: YASUDA, KAZUKI
; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,694A
; FILING DATE: August 19, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20 May 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30 July, 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/147,592
; FILING DATE: 5 No. 6319686ember 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US94/05747
; FILING DATE: 20 May 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MARK B. WILSON
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:140/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 186..1325
US-08-292-694A-1

Query Match 78.8%; Score 909.2; DB 3; Length 1410;
Best Local Similarity 86.7%; Pred. No. 3.7e-223;
Matches 1001; Mismatches 153; Conservative 0; Indels 0; Gaps 0;

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Qy    1 ATGGACTCCCGATCCAGATCTTCCCGGGGAGAGCCCGGGAGCCGGGCGCCCTACCTGCCGCGCCCCCGAGCGCC 60
              ||||| ||||| || |||||||| || ||||||||||||||||| || | |||||
Db  186 ATGGAGTCCCATTCAGATCTTCCGGAGAGATCCAGGCGCCTACCTGCTCTCCAGTGCT 245

Qy   61 TGCCTGCCCCCACAGCAGCGGCGGCGGCCTGGTTCCCGGCGCCGGCCGCAGCAGCCGGCAACGGC 120
              ||||| |||| ||||||||| || |||| ||||||||| |||||||||||||||
Db  246 TGCCTTCTCCCCACAGCAGCAGCTCTTGGTTCCCAACTGGGCAGAATCCGACAGCAGTAATGGC 305

Qy  121 AGCGGCCGGCTCGGAGGACGGCGCAGCTGGAGACAGCTGGAGTCCGCGCCGCCACATCTCCCGGCCATCCCGGTC 180
              || | |||| ||||||| ||| |||||||||||||||||||| |||||||||||||||||||||||||
Db  306 AGTGTGGGCTCAGAGGATCAGACAGCAGCTGGAGTCCGCGCCGCCACATCTCCGGCCATCCCTGTT 365

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              |||||||| ||| ||||||||||| ||||| || ||||| ||||||||||| || |||||
Db  366 ATCATCACCGCGTCTACTCCGTCGTGTTGTGTTGGTGGGCTTAGTGGGCAATTCTCTGGTC 425

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCACCAACATTACATATTTAAC 300
              |||||| || |||||||||||| ||||||||||||| |||||||||| |||||||||
Db  426 ATGTTTGTCATCATCCGATACACGAAGATGAAGACCGCAACCAACATCACATATTTAAC 485

Qy  301 CTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG 360
              |||||||||||||||||| |||||||| || |||||||||||||| |||| |||||||
Db  486 CTGGCTTTGGCAGATGCTTGGTTACTACCACTATGCCCTTCAGAGTGCGTCGTCTACTTG 545

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||| |||||||||||||| ||||| ||||||||| || |||||||||| |||||
Db  546 ATGAATTCTTGGCCTTTTGGGGAGATGTGCTATGCAAGATTGTCATTTCCATTGACTACTAC 605

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACACGCGTACATTGCCGTG 480
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Db  606 AACATGTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGCGTACATTGCTGTG 665

Qy  481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Db  666 TGCCACCCTGTGAAAGTTTGGACTTCCGAACACCCTTGAAAGCAAAGATCATCAACATC 725

Qy  541 TGCATCTGGCTGTCGTGTCATCGTGGCATCTGTGTGAATAGTCCTTGGAGGCACCCAAA 600
              |||||||||||| | |||||| || |||||| || |||||||||||||||||||||||
Db  726 TGCATTTGGCTCCTGGCATCATCGTTCGTATATCAGCGGATAGTCCTTGGAGGCACCCAAA 785

Qy  601 GTCAGGGAAGACCTCGATGTCATTGATGTCGATCTCCTTGCAGTTCCAGTGACGTACCTCC 660
              |||||||||| | || |||||||||||||  || |||| ||||| || ||| |||||||
Db  786 GTCAGGGAAGAATGTGGATGTCATTGATGTCTCGTTCCTGCAGTTTCCTGATGAATATTCC 845

Qy  661 TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTGCCTCGTCATCTTGCCTTCTCC 720
              ||||||||| |||||||||||||| || | ||||| ||||| | ||||| ||| ||||
Db  846 TGGTGGGATCTCTTCATGAAGATCTGTGTTCGTCTTTGCCTTTGCCTTTGCTTGTCCTC 905

Qy  721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
              |||||||| ||||||||||| |||||||||||||||| |||||||| ||||||||||| |||
Db  906 ATCATCATTGTCTGCTACACCCCTGATGATCCTGCGCCCTGAAGAGTGTCCGGCTCCTGTCT 965

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGGATCACCAGGACTACTCC 840
              |||||||||||||| || || || || ||  ||| |||| ||| || |||| ||| |||
Db  966 GGCTCCCGAGAGAAGACCGAAATCTCCGCCGCCGCCATCACAACCAAGTGGTGCTGGTAGTAGTT 1025

Qy  841 GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG 900
              ||||||||| || ||| || |||||||||||||||| || ||||||||||||||| ||
Db 1026 GCAGTCTTCATCATCGTTGGACCCCCATTCACATCTTATCCTGGTGGAGGCTCTCGGA 1085

Qy  901 AGCACCTTCCCAACAGCACGTCTCTCTCCAGCTATTACACTTCTGCATCGCCTTAGGCTAT 960
              |||||||||||||||||| ||| ||| ||||||||| | || || ||| |||| ||||
Db 1086 AGCACCTTCCCAACAGCACAGCTGCCTCTCCCAGCTATTATTTCTGTATTCTGGGGTTAT 1145

Qy  961 ACCAACAGTAGCCGAATCCCATTCTTCTACGCCTTCTTGATGAAATTTCAAGCGGTGT 1020
              |||||||| ||||  || || ||||| ||||||||  | |||||| |||||||||||
Db 1146 ACCAACAGCAGCCTGAATCCTGTTCTCTATGCCTTTCTCGGATGAAAACTTCAAGCGGTGT 1205

Qy 1021 TTCCGGGACTTCTGCTTCACTGAAGATGAGGACCGGCAGCGGCACTAGCAGAGTC 1080
              || | ||||| |||||||| |||| ||||| || ||| || |||| || |||| ||
Db 1206 TTTAGGGACTTGCTTCCCTTATTAAGATGAATGGAGGCACCAATAGAGTT 1265

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGACTAAAACCAGTA 1140
              ||| |||||||||||||||||||||| || |||||||||| ||||| | |||||||||
Db 1266 AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGAGATGTGGGAGGGATGAATAAGCCAGTA 1325
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Qy    1141 TGACTAGTCGTGGA 1154
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Db    1326 TGACTAGTCGTGGA 1339
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RESULT 11
US-08-147-592A-11
; Sequence 11, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
;   APPLICANT: Bell, Graeme I
;   APPLICANT: Reisine, Terry
;   APPLICANT: Yasuda, Kazuki
;   TITLE OF INVENTION: Opioid Receptor Genes,
;   TITLE OF INVENTION: Compositions and Methods
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 72210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/147,592A
;   FILING DATE: 05-NOV-1993
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30-JUL-1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20-MAY-1993
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:105
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;   NAME/KEY: N
;   LOCATION: 607-608, 642-643, 896, 906
;   IDENTIFICATION METHOD: N = A, C, G or T
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 102..986
;   FEATURE:
;   NAME/KEY: Xaa
;   LOCATION: 169, 181, 265, 269
;   IDENTIFICATION METHOD: Xaa = unknown
US-08-147-592A-11

Query Match   75.4%; Score 869.6; DB 3; Length 1000;
Best Local Similarity 97.5%; Pred. No. 4.5e-213;
Matches 891; Mismatches 0; Conservative 0; Indels 20; Gaps 3;

Qy 244 TTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACCTG 303
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Db   87   TTCTTTCTTTAGATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACCTG 146

Qy 304 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 363
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Db 147 GCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATG 206

Qy 364 AATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 207 AATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAC 266

Qy 424 ATGTTCACCAGCATCTTCACCTGACCATGATGAGCGTGACCGCTCACATTGCCGTGTGC 483
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 267 ATGTTCACCAGCATCTTCACCTGACCATGATGAGCGTGACCGCTCACATTGCCGTGTGC 326

Qy 484 CACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 543
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 327 CACCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGC 386

Qy 544 ATCTGGCTGCTGTGTCGATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC 603
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 387 ATCTGGCTGCTGTGTCGATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTC 446

Qy 604 AGGGAAGACGTCGATGTCATTGAGTGGCTCCTCGAGTTCCCAGATGATGACTACTCCTGG 663
         |||||||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Db 447 AGGGAAGGTGCGATGTCATTGAGTGGCTGCTTGCAGTTCCCAGATGATGACTACTCCTGG 506

Qy 664 TGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATC 723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 507 TGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATC 566

Qy 724 ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTCTGGC 783
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Db 567 ATCATCGTCTACACCCTGATGATCCTGCGTCTCAAGANNGTCCGGCTCCTTCTGGC 626

Qy 784 TCCCGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGGCA 843
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Db 627 TCCCGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGGCA 686

Qy 844 GTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGGAGC 903
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Db 687 GTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCGGGGAGC 746

Qy 904 ACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCTATTACTTAGGCTATACC 963
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 747 ACCTCCCACAGCACAGCTGCTTCTCCAGCTATTACTTCTGCATCGCTATTACTTAGGCTATACC 806

Qy 964 AACAGTAGCTGAATCCCATTCTCTCACGCCTTCTTCTTGATGAAAATTCAAGCGGTGTTTC 1023
         |||||||| |||||||||| |||||| ||||||||||||||||||| ||||||||||||
Db 807 AACAGTAGCCTGAATCCCATTTCTCTACGCCTTCTTCTTGATGAAAACTTCAAGCGGTGTTTC 866

Qy 1024 CGGGACTTCTGCTTCTGCTTCCACTGAAGATGAGGATGAGGCGGCAGAGCACTAGCAGAGTCCGA 1083
         ||||||||||||||||||||||||||||||||| ||| |||| |||||||||||||||||||
Db 867 CGGGACTTCTGCTTCTGCTTCCACTGAAGATGAGAATGGAGCGCNAGAGCACTAGCAGAGTCCGA 926

Qy 1084 AATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATG---GATGAATAAACCAGTA 1140
         ||||||||||||||||||||||||||||||||| ||||||| |||||||||||||||
Db 927 AATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGATGATGAATAAACCAGTA 986

Qy 1141 TGACTAGTCGTGGA 1154
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Db 987 TGACTAGTCGTGGA 1000
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RESULT 12
US-08-292-694A-11
; Sequence 11, Application US/08292694A
; Patent No. 6319686
; GENERAL INFORMATION:
;   APPLICANT: BELL, GRAEME
;   APPLICANT: REISINE, TERRY
;   APPLICANT: YASUDA, KAZUKI
;   TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

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Qy    424  ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTACATTGCCGTGTGC  483
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Db    267  ATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTACATTGCCGTGTGC  326

Qy    484  CACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC  543
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327  CACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGC  386

Qy    544  ATCTGGCTGCGTCGTCATCGTGTGGCATCTCTGCAAATAGTCCTTGGAGGCACCAAAGTC  603
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387  ATCTGGCTGCGTCGTCATCGTGTGGCATCTCTGCAAATAGTCCTTGGAGGCACCAAAGTC  446

Qy    604  AGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCCTGG  663
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447  AGGGAAGTGTCGATGTCATTGAGTGCTGCTGCTTCCCAGATGACTACTCCTGG  506

Qy    664  TGGGACCCTTCATGAAGATCTGGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATC  723
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507  TGGGACCCTTCATGAAGATCTGGGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATC  566

Qy    724  ATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGC  783
                |||||||||||||||||||||||||||||||       |||||||||||||||||||||
Db    567  ATCATCGTCTGCTACACCCCTGATGATCCTGCGTCTCAAGAGNNGTCCGGCTCCTTTCTGGC  626

Qy    784  TCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCA  843
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627  TCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCA  686

Qy    844  GTCTTCGTCGTCTGCTGACTCCATTCCATTCACATATTCATCCTGTGGGACGTCTGGGGAGC  903
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    687  GTCTTCGTCGTCTGCTGACTCCATTCCATTCACATATTCATCCTGTGGGACGTCTGGGGAGC  746

Qy    904  ACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATGCCCTTAGGCTATACC  963
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    747  ACCTCCCACAGCACAGCTGCTCTCTCCCAGCTATTACTTCTGCATGCCCTTAGGCTATACC  806

Qy    964  AACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTCAAGCCGGTGTTTC  1023
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    807  AACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAACTTCAAGCCGGTGTTTC  866

Qy    1024 CGGGACTTCTGCTTCCACTGAAGATGAGGATGGCGGCCAGAGCACTAGCAGAGTCCGA  1083
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    867  CGGGACTTCTGCTTCCACTGAAGATGAGNATCGAGCGCNAGAGCCGCNAGAGCACTAGCAGAGTCCGA  926

Qy    1084 AATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGG---GATGAATAAACCAGTA  1140
                |||||||||||||||||||                   |||||||||||||||||||||
Db    927  AATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATGAATGAATAAACCAGTA  986

Qy    1141 TGACTAGTCGTGGA  1154
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Db    987  TGACTAGTCGTGGA  1000
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RESULT 13
US-08-430-286A-1
; Sequence 1, Application US/08430286A
; Patent No. 6225080
; GENERAL INFORMATION:
;   APPLICANT: Uhl, George R.
;   APPLICANT: Eppler, C. Mark
;   APPLICANT: Wang, Jai-Bel
;   TITLE OF INVENTION: Mu-Subtype Opioid Receptor
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Darby & Darby PC
;   STREET: 805 Third Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: US
;   ZIP: 10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

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; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/292,694A
;   FILING DATE: August 19, 1994
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/066,296
;   FILING DATE: 20 May 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/100,694
;   FILING DATE: 30 July, 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: 08/147,592
;   FILING DATE: 5 No. 6319686ember 1993
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: PCT/US94/05747
;   FILING DATE: 20 May 1994
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: MARK B. WILSON
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: ARCD:140/WIM
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (713) 789-2679
;   TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: N
;   LOCATION: 607-608, 642-643, 896, 906
;   IDENTIFICATION METHOD: N = A, C, G or T
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 102..986
;   FEATURE:
;   NAME/KEY: Xaa
;   LOCATION: 169, 181, 265, 269
;   IDENTIFICATION METHOD: Xaa = unknown
US-08-292-694A-11

Query Match   75.4%; Score 869.6; DB 3; Length 1000;
Best Local Similarity 97.5%; Pred. No. 4.5e-213;
Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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        COMPUTER:  IBM PC compatible
        OPERATING SYSTEM:  PC-DOS/MS-DOS
        SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/430,286A
        FILING DATE:  28-APR-1995
        CLASSIFICATION:  536
    ATTORNEY/AGENT INFORMATION:
        NAME:  Robinson, Joseph R.
        REGISTRATION NUMBER:  33,448
        REFERENCE/DOCKET NUMBER:  0646/1A843-US5
    TELECOMMUNICATION INFORMATION:
        TELEPHONE:  212-527-7700
        TELEFAX:  212-753-6237
        TELEX:  236687
    INFORMATION FOR SEQ ID NO: 1:
        SEQUENCE CHARACTERISTICS:
        LENGTH:  2135 base pairs
        TYPE:  nucleic acid
        STRANDEDNESS:  single
        TOPOLOGY:  linear
        MOLECULE TYPE:  cDNA to mRNA
        ORIGINAL SOURCE:
        ORGANISM:  Rattus rattus
        IMMEDIATE SOURCE:
        CLONE:  mu receptor cDNA
US-08-430-286A-1
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Matches 668;   Conservative 0;   Mismatches 321;   Indels   9;   Gaps   2;
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Qy  890 AGGCCTGGGAGGCACCTCCCACAGCACAGCAGTGCTCTCCCAGCATTACTTCTGCATCG 949

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Qy  1010 TCAAGCGGTGTTTCCGGACTTCTGCTTTCCACTGAAAGATGAGGATGGCAGAGCA 1069

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; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;   APPLICANT: Yu, Lei
;   TITLE OF INVENTION:  Mu Opioid Receptors: Compostions and Methods
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Arnold, White & Durkee
;     STREET:  P. O. Box 4433
;     CITY:  Houston
;     STATE:  TX
;     COUNTRY:  USA
;     ZIP:  77210-4433
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/889,108
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/305,518
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Wilson, Mark B.
;     REGISTRATION NUMBER:  37,259
;     REFERENCE/DOCKET NUMBER:  INDA005\WIM
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  512-418-3000
;     TELEFAX:  512-474-7577
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1618 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (cDNA)
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  214..1410
US-08-889-108-1
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; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
;   APPLICANT: Yu, Lei
;   TITLE OF INVENTION: Mu Opioid Receptors: Compostions and Methods
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/889,108
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/305,518
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
;   REFERENCE/DOCKET NUMBER: INDA005\WIM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1618 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (cDNA)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 339..1235
US-08-889-108-3

Query Match   38.5%; Score 444.8; DB 3; Length 1618;
Best Local Similarity 66.8%; Pred. No. 4.9e-104;
Matches 667; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

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Job time : 218 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1152.4	99.9	1602	19	US-10-278-698-45	Sequence 45, Appl
4	1152.4	99.9	1602	19	US-10-278-698-559	Sequence 559, App
5	1150.8	99.7	1154	11	US-09-904-584-2	Sequence 2, Appli
6	1150.8	99.7	1154	11	US-09-904-584-3	Sequence 3, Appli
7	1150.8	99.7	1154	11	US-09-904-584-5	Sequence 5, Appli
8	1150.8	99.7	1154	11	US-09-904-584-6	Sequence 6, Appli
9	1150.8	99.7	1154	11	US-09-904-584-7	Sequence 7, Appli
10	1144.4	99.2	1182	15	US-10-225-567A-147	Sequence 147, Appl
11	1144.4	99.2	1182	15	US-10-345-680-19	Sequence 19, Appl

12	1144.4	99.2	1182	17	US-10-305-720-1417	Sequence 1417, Ap
13	1144.4	98.9	1182	18	US-10-283-975A-80	Sequence 80, Appl
14	1141.4	98.9	1143	16	US-10-318-661-1	Sequence 1, Appli
15	1136.2	98.5	1284	16	US-10-318-661-3	Sequence 3, Appli
16	1133.4	98.2	1143	15	US-10-345-680-21	Sequence 21, Appl
17	1130.2	97.9	1143	10	US-09-826-509-542	Sequence 542, App
18	1130.2	97.9	1143	19	US-10-925-095-542	Sequence 542, App
19	999.6	86.6	1275	16	US-10-318-661-5	Sequence 5, Appli
20	994.6	86.2	1275	16	US-10-318-661-7	Sequence 7, Appli
21	979.4	84.9	1875	16	US-10-318-661-13	Sequence 13, Appl
22	963.4	83.5	1875	16	US-10-318-661-15	Sequence 15, Appl
23	909.2	78.8	1408	9	US-09-214-904-5	Sequence 5, Appli
24	877.8	76.1	1911	16	US-10-318-661-17	Sequence 17, Appl
c 25	469	40.6	585	13	US-10-027-632-188121	Sequence 188121,
c 26	469	40.6	585	13	US-10-027-632-188122	Sequence 188122,
c 27	469	40.6	585	17	US-10-027-632-188121	Sequence 188121,
c 28	469	40.6	585	17	US-10-027-632-188122	Sequence 188122,
29	444.8	38.5	1618	10	US-09-841-720-1	Sequence 1, Appli
30	444.8	38.5	1618	19	US-09-841-720-3	Sequence 3, Appli
31	434.6	37.7	1464	14	US-10-185-083-25	Sequence 25, Appl
32	433.2	37.5	1239	14	US-10-080-917-10	Sequence 10, Appl
33	433.2	37.5	1245	14	US-10-080-917-8	Sequence 8, Appli
34	433.2	37.5	1388	14	US-10-185-083-26	Sequence 26, Appl
35	433.2	37.5	1431	14	US-10-080-917-6	Sequence 6, Appli
36	433.2	37.5	2149	14	US-10-080-917-12	Sequence 12, Appl
37	433.2	37.5	2162	11	US-09-883-839-1	Sequence 1, Appli
38	433.2	37.5	2162	11	US-09-883-839-3	Sequence 3, Appli
39	433.2	37.5	2162	11	US-09-883-839-5	Sequence 5, Appli
40	433.2	37.5	2162	15	US-10-225-567A-185	Sequence 185, App
41	433.2	37.5	2162	17	US-10-305-720-1379	Sequence 1379, Ap
42	433.2	37.5	2279	19	US-10-477-714-33	Sequence 33, Appl
43	431.6	37.4	1176	10	US-09-935-061-11	Sequence 11, Appl
44	431.6	37.4	1176	18	US-10-692-071-11	Sequence 11, Appl
45	431.6	37.4	1473	14	US-10-080-917-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-904-584-4
; Sequence 4, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-4

Query Match   100.0%; Score 1154; DB 11; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCAGCGGCTGGTTTCCCGGCCCGGAGCCCGGACAGCAACGGC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
US-09-904-584-1
; Sequence 1, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-1

Query Match   99.9%;   Score 1152.4;   DB 11;   Length 1154;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1153;   Conservative 0;   Mismatches 0;   Indels 1;   Gaps 0;

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Qy     1 ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGGGCCTACCTGCGCCCCGAGCGCC    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGACTCCCGATCCAGATCTTCCGCGGGGGAGCCGGGGCCCTACCTGCGCGCCCCGAGCGCC    60

Qy    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGTCGGAGCCCGCGCACAGCAACGGC   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGCCCCCAACAGCAGCGGCCTGGTTCCCGGTCGGAGCCCGCGCACAGCAACGGC   120

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGACACTCCCGGCCATCCCGGTC   180
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGACACTCCCGGCCATCCCGGTC   180

Qy   181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGGCGGGTCTACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC   240

Qy   241 ATGTTCGTGATCATCCGATACAACATTACATATTTAAC   300
           ||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACAACATTACATATTTAAC   300

Qy   301 CTGGCTTTGGAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGGAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG   360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC   420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGGACCGTGT   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGTGGACCGTGT   480

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACTTCGTCGTCATCTGCAATAGTCCTTGCAATATC   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCATCTCGTCGTCATCTGCAATAGTCCTTGCAATATC   540

Qy   541 TGCATCTGGCTCGTCGTCGTCATCTGTTGCTAT   600
           |||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTCGTCGTCGTCATCTGTTGCTAT   600

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGTGATGATGACTACTCC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCCTTGCAGTTCCCAGTGATGATGACTACTCC   660
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Qy   181  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCAACTCGCTGGTC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556  ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCGTGGCAACTCGCTGGTC  615

Qy   241  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   616  ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC  675

Qy   301  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   676  CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG  735

Qy   361  ATGAATTCCTGGCCTTTGGGGATGGTGCGTGCAAGATAGTAATTCCATTGATTACTAC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   736  ATGAATTCCTGGCCTTTGGGGATGGTGCGTGCAAGATAGTAATTCCATTGATTACTAC  795

Qy   421  AACATGTTCACCAGCATCTTCACCTGACCGCTACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   796  AACATGTTCACCAGCATCTTCACCTGACCGCTACATTGCCGTG  855

Qy   481  TGCCACCCCGTGAAGGCTTGGACTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   856  TGCCACCCCGTGAAGGCTTGGACTCCGCACACCCTGAAGGCAAAGATCATCAATATC  915

Qy   541  TGCATCTGGCTGGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   916  TGCATCTGGCTGGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  975

Qy   601  GTCAGGGAGACGTCGATGTCATGAGTGCTCCCAGTACTGACTACTCC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   976  GTCAGGGAGACGTCGATGTCATGAGTGCTCCCAGTACTGACTACTCC  1035

Qy   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC  1095

Qy   721  ATCATCATCGTCTGCTACACACCCTGCGGTCTCAAGAGCGTCCGGCTCCTTTCT  780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 ATCATCATCGTCTGCTACACACCCTGCGGTCTCAAGAGCGTCCGGCTCCTTTCT  1155

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCGCCTGGTCTCTGGTGTGGTGGTG  840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCGCCTGGTCTCTGGTGTGGTGGTG  1215

Qy   841  GCAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG  1275

Qy   901  AGCACCTCCACAGCACAGCCTGCTCTCTCCAGCTATTACTTCTGATGAAAATTTCAAGCGGGTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AGCACCTCCACAGCACAGCCTGCTCTCTCCAGCTATTACTTCTGATGAAAATTTCAAGCGGGTAT  1335

Qy   961  ACCAACAGTAGCCTGAATCCCATTCTCACTGAAGATGAGCGGCGAGTC  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 ACCAACAGTAGCCTGAATCCCATTCTCACTGAAGATGAGCGGCGAGTC  1395

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGGATCTCGTTTCCACTGAAGATGGAGGAACCAGTA  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 TTCCGGGACTTCTGCTTTCCACTGGATCTCGTTTCCACTGAAGATGGAGGACCAGTA  1455

Qy   1081 CGAAATACAGTTCAGGATCTCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CGAAATACAGTTCAGGATCTCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1515

Qy   1141 TGACTAGTCGTGGA  1154
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Db   1516 TGACTAGTCGTGGA  1529
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RESULT 4
US-10-278-698-559
; Sequence 559, Application US/10278698

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Qy   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGTCCTC  720
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Db   661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGTCCTC  720

Qy   721  ATCATCATCGTCTGCTACACACCCTGCGGTCTCAAGAGCGTCCGGCTCCTTTCT  780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATCATCATCGTCTGCTACACACCCTGCGGTCTCAAGAGCGTCCGGCTCCTTTCT  780

Qy   781  GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCGCCTGGTCTCTGGTGGTGGTG  840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCCGCCTGGTCTCTGGTGGTGGTG  840

Qy   841  GCAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCAGTCTTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTGGAGGGCTCTGGGG  900

Qy   901  AGCACCTCCACAGCACAGCCTGCTCTCTCCAGCTATTACTTCTGATGAAAATTTCAAGCGGGTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AGCACCTCCACAGCACAGCCTGCTCTCTCCAGCTATTACTTCTGATGAAAATTTCAAGCGGGTAT  960

Qy   961  ACCAACAGTAGCCTGAATCCCATTCTCACTGAAGATGAGCGGCGAGTC  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  ACCAACAGTAGCCTGAATCCCATTCTCACTGAAGATGAGCGGCGAGTC  1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGGATCTCGTTTCCACTGGATCTCGTTTCCCGGGCCGC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGGATCTCGTTTCCACTGGATCTCGTTTCCCGGGCCGC  1080

Qy   1    ATGGAGACTCCCCGATCCCCGATCTTCCGCGGGAGCGGGAGCCCTACCTGCGCCCGAGCGCC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   376  ATGGAGACTCCCCGATCCCCGATCTTCCGCGGGAGCGGGAGCCCTACCTGCGCCCGAGCGCC  435

Qy   61   TGCCTGCCCCCCAACAGCAGCGGCGCCTGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   436  TGCCTGCCCCCACAGCAGCGGCGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC  495

Qy   121  AGGCGCCGCTCGGAGGAGACGCGCAGCTGAGCTCGGCGACATCTCCCCGGCCATCCCGGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   496  AGCGCCCGCTCGGAGGAGACGCGCAGCTGAGCTCGGCGACATCTCCCCGGCCATCCCGGTC  555
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RESULT 3
US-10-278-698-45
; Sequence 45, Application US/10278698
; Publication No. US2005003734A1
; GENERAL INFORMATION:
;   APPLICANT: PathoArray GmbH
;   APPLICANT: Stuhlmuller, Bruno
;   APPLICANT: Haupl, Thomas
;   TITLE OF INVENTION: Nucleic Acid Array
;   FILE REFERENCE: O30027US
;   CURRENT APPLICATION NUMBER: US/10/278,698
;   CURRENT FILING DATE: 2002-10-23
;   NUMBER OF SEQ ID NOS: 1050
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1602
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-278-698-45
Query Match   99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1153; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: PathoArray GmbH
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-559

Query Match   99.9%;   Score 1152.4;   DB 19;   Length 1602;
Best Local Similarity 99.9%; Pred. No. 0;   Gaps   0;
Matches 1153; Conservative   0; Mismatches   1; Indels   0;

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  376 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 435

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCCGAGCCCGACAGCAGCAACGGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  436 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCCGAGCCCGACAGCAGCAACGGC 495

Qy  121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCGCCGCACATCTCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  496 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCGCCGCACATCTCCCGGCCATCCCGGTC 555

Qy  181 ATCATCACGCGCGGTCTACTCCGTAGTGTTCGTGTGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  556 ATCATCACGCGCGGTCTACTCCGTAGTGTTCGTGTGGCAACTCGCTGGTC 615

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  616 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 675

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  676 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 735

Qy  361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  736 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 795

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
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Db  796 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 855

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  856 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 915

Qy  541 TGCATCTGGCTGCTCTGTCATCTGTTGGCATCTTCTGCAATAGTCCTTGGAGGCACCAAA 600
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Db  916 TGCATCTGGCTGCTCTGTCATCTGTTGGCATCTTCTGCAATAGTCCTTGGAGGCACCAAA 975

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  976 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 1035

Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1036 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTC 1095

Qy  721 ATCATCACGCGGTCTACTCCGTAGTGTTCGTGTGGCGGCTTCGTGGTGGTGGCAACTCGCTGGTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1096 ATCATCACGCGGTCTACTCCGTAGTGTTCGTGTGGCGGCTTCGTGGTGGTGGCAACTCGCTGGTCT 1155
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Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCTGTAGGATCACCAGACTGGTCCTCGTGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1156 GGCTCCCGAGAGAAAGATCGCAACCTGCTGTAGGATCACCAGACTGGTCCTCGTGGTGGTGGTG 1215

Qy  841 GCAGTCTTCGTCGTCTGCTGCTGCCCATTCCATTCACATATTCATCCTGTGGAGGCTCTGGGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1216 GCAGTCTTCGTCGTCTGCTGCTGCCCATTCCATTCACATATTCATCCTGTGGAGGCTCTGGGG 1275

Qy  901 AGCAACTCCACCAGCAGCAGTGCTCCAGTCTGCTCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1276 AGCAACTCCACCAGCAGCAGTGCTCCAGTCTGCTCTTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 1335

Qy  961 ACCAACAGTAGCCTGAATCCCATTCCTCCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1336 ACCAACAGTAGCCTGAATCCCATTCCTCCTACGCCTTTCTTGATGAAAACTTCAAGCGGTGT 1395

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1396 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1455

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1456 CGAAATACAGTTCAGGATCCTGCTTACCTGACGGGACATCGATGGGATGAATAAACCAGTA 1515

Qy 1141 TGACTAGTCGTGGA 1154
          ||||||||||||
Db 1516 TGACTAGTCGTGGA 1529
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RESULT 5
US-09-904-584-2
; Sequence 2, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;   Gaps   0;
Matches 1152; Conservative   0; Mismatches   2; Indels   0;

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCCGAGCCCGACAGCAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTTCCCGGCCCGAGCCCGACAGCAGCAACGGC 120

Qy  121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCGCCGCACATCTCCCGGCCATCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCGCCGCACATCTCCCGGCCATCCCGGTC 180

Qy  181 ATCATCACGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGTGGTGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGGTGGTGGCAACTCGCTGGTC 240
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; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-3

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1152;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   0;

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Qy    1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCGGCCCTACCTCGCCCCCGAGCGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCGGCCCTACCTCGCCCCCGAGCGCGCC 60

Qy   61 TGGCTGCCCCCAACAGCAGCGCGCCCTGGTTCCCGCTGGCGCCGAGCGCCGAGCAGCAACGGC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGGCTGCCCCCAACAGCAGCGCGCCCTGGTTCCCGCTGGCGCCGAGCGCCGAGCAGCAACGGC 120

Qy  121 AGGCCCGGCTCGGAGGACGCGCAGCTGAGCCGCGCCCGCGCCCGCCCGCCCATCCCGGTC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGGCCCGGCTCGGAGGACGCGCAGCTGAGCCGCGCCCGCGCCCGCCCGCCCATCCCGGTC 180

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTCGGCTTGGTGGGCAACTCGCTGGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTCGGCTTGGTGGGCAACTCGCTGGTC 240

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTCTGTCAAGATAGTAATTTCCATTGATTACTAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTTGGGGATGTCTGTCAAGATAGTAATTTCCATTGATTACTAC 420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACCCCTGAAGGCAAAGATCATCAATATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACCCCTGAAGGCAAAGATCATCAATATC 540

Qy  541 TGCATCTGGCTGCTGTCGTCATCTGTTGCAATAGTCCTTGGAGGCACCACCAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTCATCTGTTGCAATAGTCCTTGGAGGCACCACCAA 600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTCCTTGCGAGTGAGTTCCCAGATGTCATT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTCCTTGCGAGTGAGTTCCCAGATGTCATT 660

Qy  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTC 720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTACACCCTGATGATCCTGCGTCTTTCT 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTACACCCTGATGATCCTGCGTCTTTCT 780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGGATGGTCGTGGTG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCCTAGGATCACCAGGATGGTCGTGGTG 840
```

Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 GCAGTCTTCGTCTGCTGGACTCCATTCATCCTGCTATTACTTCTGCAGTGAGGCTCTGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCTGCTGGACTCCCATTCCATTCATCCTGGTATTACTTCTGGTGGAGGCTCTGGGG 900

Qy   901 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCGTGT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCGTGT 960

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCAGATCTTCCGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCAGATCTTCCGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154

RESULT 7
US-09-904-584-5
; Sequence 5, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 5
;   LENGTH: 1154
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-904-584-5

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1152;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCCGGGGAGCCCTACCTGCGCCCCGAGCGGC 60
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCCGGGGAGCCCTACCTGCGCCCCGAGCGGC 60

Qy   61 TGCCTGCGCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCTGGCCGGAGCAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCCTGCGCCCCAACAGCAGCGCCTGGTTTCCCGGCTGGGCCTGGCCGGAGCAGCAACGGC 120

Qy   121 AGCGGCCGGCTCGGAGGACGCGGGAGGACGCGGCCGGCCCGGCCACATCTCCCGGCCATCCCGGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCGGCCGGCTCGGAGGACGCGGGAGGACGCGGCCGGCCCGGCCACATCTCCCGGCCATCCCGGGTC 180

Qy   181 ATCATCACGCGCGGTCTACTCCGTAGTGTTCGTCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATCATCACGCGCGGTCTACTCCGTAGTGTTCGTCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC 240

Qy   241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAAC 300

Qy   301 CTGGCTTTGCAGATGCTTTAGTTACTACAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGCTTTGCAGATGCTTTAGTTACTACAGAGTACGGTCTACTTG 360

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTGCCGTG 480

Qy   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540

Qy   541 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600

Qy   601 GTCAGGGAAGACGTCGATGCTCATTGAGTGAGTGTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCAGGGAAGACGTCGATGCTCATTGAGTGAGTGTCCCAGATGATGACTACTCC 660

Qy   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCTTGCCTTGCCTGTCCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCGTCTTGCCTTGCCTGTCCTC 720

Qy   721 ATCATCATCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGTCCGGCTCCTTTCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCATCATCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGTCCGGCTCCTTTCT 780

Qy   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGCTGGTG 840

Qy   841 GCAGTCTTCGTCTGCTGGACTCCATTCATCCTGCTATTACTTCTGCAGTGAGGCTCTGGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCAGTCTTCGTCTGCTGGACTCCATTCATCCTGCTATTACTTCTGCAGTGAGGCTCTGGGG 900

Qy   901 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGCACCTCCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATGCCTTAGGCTAT 960

Qy   961 ACCAACAGTAGCCTGAATCCAATCCATTCCTTCTTGATGAAATTCAAGCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCAACAGTAGCCTGAATCCAATCCATTCCTTCTTGATGAAATTCAAGCGGTGT 1020

Qy   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy   1081 CGAAATACAGTTCAGGATCCAGATCTTCCGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGAAATACAGTTCAGGATCCAGATCTTCCGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy   1141 TGACTAGTCGTGGA 1154
          ||||||||||||||
Db   1141 TGACTAGTCGTGGA 1154

RESULT 8
US-09-904-584-6
; Sequence 6, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid

```
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-6

Query Match             99.7%;     Score 1150.8;     DB 11;     Length 1154;
Best Local Similarity   99.8%;     Pred. No. 0;
Matches 1152;  Conservative    0;  Mismatches    2;  Indels     0;  Gaps     0;

Qy          1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCGCCCGAGCACGAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCGCCCGAGCACGAGCAACGGC 120

Qy        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180

Qy        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy        241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy        421 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480

Qy        481 TGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCCTTCGAATAGTCCTTGGAGGCACCAAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCCTTCGAATAGTCCTTGGAGGCACCAAA 540

Qy        541 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCGCATCTCTGCAATAGTCCTCGCAATAGTCCTCGTACTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCGCATCTCTGCAATAGTCCTCGCAATAGTCCTCGTACTCC 600

Qy        601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660

Qy        661 TGGTGGGAACCTTCATGAAGATCTCGCGTCTCAAGAGCGTCTCAAGAGCGTCCGTCTTGTCTCTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGTGGGAACCTTCATGAAGATCTCGCGTCTCAAGAGCGTCTCAAGAGCGTCCGTCTTGTCTCTC 720

Qy        721 ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCCGTCTCAAGAGCGTCTCCGGCTCCTTTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATCATCACGTCTGCTACACCCTGATGATCCTGCGTCCGTCTCAAGAGCGTCTCCGGCTCCTTTCT 780

Qy        781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTCGTGGTG 840
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RESULT 9
US-09-904-584-7
; Sequence 7, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-7

Query Match   99.7%;   Score 1150.8;   DB 11;   Length 1154;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1152; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy          1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCGCCCGAGCCACGAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCGCCCGAGCCACGAGCAACGGC 120

Qy        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180

Qy        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGTC 240

Qy        241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300

Qy        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Db        301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360

Qy        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Qy        421 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACATGTTCACCAGCATCTTCACCCTTGACCATGATGAGCCGTGGACCGCTACATTGCCGTG 480

Qy        481 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCATCTCTGCAGTAGTCTTGGAGGCACCAAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCATCTCTGCAGTAGTCTTGGAGGCACCAAA 540

Qy        541 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCATCTCTGCAGTAGTCTTGGAGGCACCAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCATCTGGCTGCTCGTGTGCATCTCGGTCTGCATCTCTGCAGTAGTCTTGGAGGCACCAAA 600

Qy         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCCCCGAGCCACGAGCAACGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCTGCCCCAACAGCAGCGCGCTGGTTTCCCGGCCCCGAGCCACGAGCAACGGC 120

Qy        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCGCCGGCTCGGAGGACGCGCAGCTCGGAGCGCGCACATCTCCCCGGCCATCCCCGGTC 180

Qy        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGTC 240

Qy        241 ATGTTCGTGATCATCCGATACAACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Allelles, and

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Db        781 GCAGTCTTCGTCGTGCTGCTGGACTCCCATTCACATATTATTCATCCTGGTGAGGCTCGGG 900
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCGGTCTTCGTCGTGCTGCTGGACTCCCATTCACATATTATTCATCCTGGTGAGGCTCGGG 900

Qy        901 AGCACCTCCACAGCACAGCACAAGCTGCTCTCCAGCTATTACTTCTGCATCGCATCGCCTTAGGCTAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGCACCTCCACAGCACAGCACAAGCTGCTCTCCAGCTATTACTTCTGCATCGCATCGCCTTAGGCTAT 960

Qy        961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCCTTTCTGATGAAAATTTCAAGCGGTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCCTTTCTGATGAAAACTTCAAGCGGTGT 1020

Qy       1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGAGCGGCAGAGCACTAGCAGAGTC 1080
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGAGCGGCAGAGCACTAGCAGAGTC 1080

Qy       1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140

Qy       1141 TGACTAGTCGTGGA 1154
              ||||||||||||||
Db       1141 TGACTAGTCGTGGA 1154
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;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 147
;  LENGTH: 1182
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-225-567A-147

Query Match             99.2%;  Score 1144.4;  DB 15;  Length 1182;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1148;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    1 ATGGACTCCCGATCCAGATCTTCGCGGGAGCCGGCCCTACCTGCCCGAGCCGCC  60
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   14 ATGAATCCCCGATTCAGATCTTCCGCGGCGGGAGCGCTGGCCCTACCTGCGCCCGAGCCGCC  73

Qy   61 TGCCTGCCCCCAACAGCAGCGCCCTTGGTTCCCGGCTGGGCCGAGCCGACAGCAACGGC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCAACAGCAGCGCCCTTGGTTCCCGGCTGGGCCGAGCCGACAGCAACGGC  133

Qy  121 AGCGCCGGCTCGGAGGACGCGGCAGCTGGACCCGGCCACATCTCCCGGCCATCCCGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 AGCGCCGGCTCGGAGGACGCGGCAGCTGGACCCGGCCACATCTCCCGGCCATCCCGGTC  193

Qy  181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  194 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC  253

Qy  241 ATGTTCGTGATCATCCGATACAACAAGATGAAGCAGCAGCAACATTACATATTTAAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  254 ATGTTCGTGATCATCCGATACAACAAGATGAAGCAGCAGCAACATTACATATTTAAC  313

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  373

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCAAGATAGTAATTTCCATTGATTACTAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  374 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCAAGATAGTAATTTCCATTGATTACTAC  433

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  493

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  494 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  553

Qy  541 TGCATCTGGCTGCTGTCGTGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  554 TGCATCTGGCTGCTGTCGTGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  613

Qy  601 GTCAGGGAAGACGTCCATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  614 GTCAGGGAAGACGTCCATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGACTACTCC  673

Qy  661 TGGTGGGACCTTCTCATCTTTGTCGTCTTCATCTTTGCCTTCGTCTTCATCTTTGTCCTC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  674 TGGTGGGACCTTCTCATCTTTGTCGTCTTCATCTTTGCCTTCGTCTTCATCTTTGTCCTC  733

Qy  721 ATCATCATCGTCTGCTACACCCGATGATCCTGCGCTCACAGAGCTGGTGGTGGTG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  734 ATCATCATCGTCTGCTACACCCGATGATCCTGCGCTCACAGAGCTGGTGGTGGTG  793

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  794 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCCTGGTGGTGGTG  853
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Db  241 ATGTTCGTGATCATCCGATACAACAAGATGAAGCAGCAGCAACATTACATATTTAAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG  360

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCAAGATAGTAATTTCCATTGATTACTAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ATGAATTCCTGGCCTTTTGGGGATGGTGCTGCAAGATAGTAATTTCCATTGATTACTAC  420

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG  480

Qy  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATC  540

Qy  541 TGCATCTGGCTGCTGTCGTGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGCATCTGGCTGCTGTCGTGCATCTCTGCAATAGTCCTTGGAGGCACCAAA  600

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTGCAGTGCTCCCAGATGATGACTACTCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTGCAGTGCTCCCAGATGATGACTACTCC  660

Qy  661 TGGTGGGACCTTCGTCGTCGTCCTTCATCTTTCGTCTTCGTGATCCTGTCCTC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TGGTGGGACCTTCGTCGTCGTCCTTCATCTTTCGTCTTCGTGATCCTGTCCTC  720

Qy  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGCTCCGAGAGCGTCCGGCTCCTTTCT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ATCATCATCGTCTGCTACACCCTGATGATCCTGCGCTCCGAGAGCGTCCGGCTCCTTTCT  780

Qy  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGAGGGACTGGTCCTGGTGGTGGTGGTG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GGCTCCCGAGAGAAAGATCGCAACCTGCGAGGGACTGGTCCTGGTGGTGGTGGTG  840

Qy  841 GCAGTCTTCGTCGTCGCTGGACTCCCATTCATCGTCTGGGAGAGGCTCGGGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCAGTCTTTCGTCGTCGCTGGACTCCCATTCATCGTCTGGGAGAGGCTCGGGG  900

Qy  901 AGCACCTCCCACAGACAGCTGCTCTCCCAGCGTATTACTTCTGCATCGCCTTAGGCTAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AGCACCTCCCACAGACAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTAT  960

Qy  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAATTTCAAGCGGTGT  1020

Qy 1021 TTCCCGGGACTTCTGCTTTCGCTTTCCACTGAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTCCCGGGACTTCTGCTTTCGCTTTCCACTGAGATGAGGCGGCAGAGCACTAGCAGAGTC  1080

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA  1140

Qy 1141 TGACTAGTCGTGGA  1154
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Db 1141 TGACTAGTCGTGGA  1154
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RESULT 10
US-10-225-567A-147
; Sequence 147, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

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Qy    1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGGCCGGCCGGCCCTACCTGCGCCCGAGCGCC   60
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGGCCGGCCGGCCCTACCTGCGCCCGAGCGCC   73

Qy   61 TGCCTGCCCCCACACAGCGCGCCTGGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   120
        |||||| ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   74 TGCCTGCCCCCACACAGCGCGCCTGGTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC   133

Qy  121 AGCCGGCTCGGAGGACGGCGCAGCTGGGCCGGCCCGCACATCTCCCCGGCCATCCCGGTC   180
        ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  134 AGCCGGCTCGGAGGACGGCGCAGCTGGGCCGGCCCGCACATCTCCCCGGCCATCCCGGTC   193

Qy  181 ATCATCACCGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGTGGGCAACTCGCTGGTC   240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  194 ATCATCACCGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGGTGTGGGCAACTCGCTGGTC   253

Qy  241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACCATTTACATATTTAAC   300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCACCATTTACATATTTAAC   313

Qy  301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTACTTG   360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCGTACTTG   373

Qy  361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC   433

Qy  421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG   480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG   493

Qy  481 TGCCACCCCGTGAAGGCTTGGACTTCCCCACACCCTTGAAGGCAAAGATCATCAATATC   540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  494 TGCCACCCCGTGAAGGCTTGGACTTCCCCACACCCTTGAAGGCAAAGATCATCAATATC   553

Qy  541 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA   600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  554 TGCATCTGGCTGCGTCGTCATCTGTTGGCATCTCGCAATAGTCCTTGGAGGCACCAAA   613

Qy  601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC   673

Qy  661 TGGTGGGGACTCCTTCATGAAGATCTGCCTTCGTCTTGCCTTCGTCGTCCTGTCCTC   720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  674 TGGTGGGGACTCCTTCATGAAGATCTGCCTTCGTCTTGCCTTCGTCGTCCTGTCCTC   733

Qy  721 ATCATCATCGTCTGCTACACACCCTGATGATCCTGGTCTCAAGAGCGTCCAAGAGCGTCCTTCT   780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  734 ATCATCATCGTCTGCTACACACCCTGATGATCCTGGTCTCAAGAGCGTCCAAGAGCGTCCTTCT   793

Qy  781 GGCTCCCGAGAAAGATCGCAACCTGGTAGGATCCACCAGACTGGTCCTGGTGGAGGCTCGGGTG   840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  794 GGCTCCCGAGAAAGATCGCAACCTGGTAGGATCCACCAGACTGGTCCTGGTGGAGGCTCGGGTG   853

Qy  841 GCAGTCTTCGTTCGTCTGCTGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG   900
        || ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  854 GCGGTTTTCGTTCGTCTGCTGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGG   913

Qy  901 AGCACCTCCCACAGCACAGCAGCTCCTTCTCTGCTATTACTTCTGCATCGCCTTAGGCTAT   960
        || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  914 AGCACCTCCCACAGCACAGCAGCTCCTTCTCTGCTATTACTTCTGCATCGCCTTAGGCTAT   973

Qy  961 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAAATTCAAGCGGGTGT   1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  974 ACCAACAGTAGCCTGAATCCATTCTCTACGCCTTTCTTGATGAAACTTCAAGCGGGTGT   1033

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC   1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGCACTAGCAGAGTC   1093

Qy 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGAATAAACCAGTA   1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGAATAAACCAGTA   1153

Qy 1141 TGACTAGTCGTGGA   1154
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Db 1154 TGACTAGTCGTGGA   1167
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RESULT 11
US-10-345-680-19
; Sequence 19, Application US/10345680
; Publication No. US2003014839A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNM_OMNI
; CURRENT APPLICATION NUMBER: US710/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(1156)
US-10-345-680-19

Query Match   99.2%; Score 1144.4; DB 15; Length 1182;
Best Local Similarity   99.5%; Pred. No. 0;
Matches 1148; Conservative 0; Mismatches 0; Indels 6; Gaps 0;

Db　1094　CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153
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Qy　1141　TGACTAGTCGTGGA 1154
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Db　1154　TGACTAGTCGTGGA 1167

RESULT 12
US-10-305-720-1417
; Sequence 1417, Application US/10305720
; Publication No. US2004010136A1
; GENERAL INFORMATION:
;　APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;　TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
;　FILE REFERENCE: PA-0002-1 CON
;　CURRENT APPLICATION NUMBER: US/10/305,720
;　CURRENT FILING DATE:　2002-11-26
;　PRIOR APPLICATION NUMBER: 09/016,434
;　PRIOR FILING DATE: 1998-01-30
;　NUMBER OF SEQ ID NOS: 1490
;　SOFTWARE: PERL Program
; SEQ ID NO 1417
;　LENGTH: 1182
;　TYPE: DNA
;　ORGANISM: Homo sapiens
;　FEATURE:
;　NAME/KEY: misc_feature
;　OTHER INFORMATION: GenBank ID No. US20040010136A1 g532059
US-10-305-720-1417

Query Match　　　99.2%;　Score 1144.4;　DB 17;　Length 1182;
Best Local Similarity　99.5%;　Pred. No. 0;
Matches 1148;　Conservative　0;　Mismatches　6;　Indels　0;　Gaps　0;

Qy　　　1　ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCCCAGCGGCC 60
　　　　　|||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　14　ATGGAATCCCCGATTCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCCCCCCAGCGGCC 73

Qy　　61　TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 120
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　74　TGCCTGCCCCCAACAGCAGCGGCCTGGTTTCCCGGCTGGGCCGAGCCCGACAGCAACGGC 133

Qy　121　AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCACATCTCCCCGGCCATCCGGGTC 180
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　134　AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCACATCTCCCCGGCCATCCGGGTC 193

Qy　181　ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTCGTCGTGGGCAACTCGCTGGTC 240
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　194　ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGGCTTCGTCGTGGGCAACTCGCTGGTC 253

Qy　241　ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　254　ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313

Qy　301　CTGGCTTTGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　314　CTGGCTTTGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 373

Qy　361　ATGAATTCCTGGCCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　374　ATGAATTCCTGGCCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy　421　AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACGCGCTACATTGCCGTG 480
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　434　AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACGCGCTACATTGCCGTG 493

Qy　481　TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　494　TGCCACCCCGTGAAGGCTTTGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy　541　TGCATCTGGCTGCTGCTCGTGCTGTTGGCATCCTGCTGCAATAGTCCTTGGAGGCACCAAA 600
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db　554　TGCATCTGGCTGCTGCTCGTGCTGTTGGCATCCTGCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy　601　GTCAGGGAAGACGTCGATGTCATTGAGTGCTGTCCTTGCAGTTCCCAGATGATGACTACTCC 660
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　614　GTCAGGGAAGACGTCGATGTCATTGAGTGCTGTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy　661　TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTGCCTTCGTGATCCCGTCCTC 720
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　674　TGGTGGGACCTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTGCCTTCGTGATCCCGTCCTC 733

Qy　721　ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGGTCCGGCTCCTTTCT 780
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　734　ATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGGGTCCGGCTCCTTTCT 793

Qy　781　GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGACTACCAGACTGGTCCTGGTGGTGGTG 840
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　794　GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTG 853

Qy　841　GCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCTCGTGGAGGCTCTGGGG 900
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　854　GCGGTTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCTCGTGGAGGCTCTGGGG 913

Qy　901　AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGATGAAATTCTCAAGCGTAT 960
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　914　AGCACCTCCCACAGCACAGCTGCTCTCCAGCTATTACTTCTGATGAAATTCTCAAGCGTAT 973

Qy　961　ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTACGCCTTTCTGATGAAAACTTCAAGCCGGTGT 1020
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　974　ACCAACAGTAGCCTGAATCCCATTCTTCTACGCCTTTCTACGCCTTTCTGATGAAAACTTCAAGCCGGTGT 1033

Qy　1021　TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1034　TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1093

Qy　1081　CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1094　CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy　1141　TGACTAGTCGTGGA 1154
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Db　1154　TGACTAGTCGTGGA 1167

RESULT 13
US-10-283-975A-80
; Sequence 80, Application US/10283975A
; Publication No. US2004011079Z A1
; GENERAL INFORMATION:
;　APPLICANT: Ortho-Clinical Diagnostics, Inc.
;　TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
;　FILE REFERENCE: CDS 293 PCT
;　CURRENT APPLICATION NUMBER: US/10/283,975A
;　CURRENT FILING DATE:　2002-10-30
;　PRIOR APPLICATION NUMBER: 60/340,938
;　PRIOR FILING DATE: 2001-10-30
;　PRIOR APPLICATION NUMBER: 60/338,997
;　PRIOR FILING DATE: 2001-10-30
;　PRIOR APPLICATION NUMBER: 60/340,081
;　PRIOR FILING DATE: 2001-10-30
;　PRIOR APPLICATION NUMBER: 60/341,012
;　PRIOR FILING DATE: 2001-10-30
;　NUMBER OF SEQ ID NOS: 900
;　SOFTWARE: Patentin version 3.1
; SEQ ID NO 80
;　LENGTH: 1182
;　TYPE: DNA
;　ORGANISM: HUMAN
US-10-283-975A-80

Query Match　　　99.2%;　Score 1144.4;　DB 18;　Length 1182;
Best Local Similarity　99.5%;　Pred. No. 0;
Matches 1148;　Conservative　0;　Mismatches　6;　Indels　0;　Gaps　0;

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Qy      1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
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Db     14 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGGCCGGGCCCTACCTGCGCCCCGAGCGCC 73

Qy     61 TGCCTGCCCCCAACAGCAGCAGCGCGCGACGCTGAGCCCGCACATCTCCCCGGCCATCCCGGTC 120
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Db     74 TGCCTGCCCCCAACAGCAGCAGCGCGCGACGCTGAGCCCGCACATCTCCCCGGCCATCCCGGTC 133

Qy    121 AGGCCGGCTCGGAGGACGACGCGCGACGCTGAGCCCGCAGCTGAGCCCGCACATCTCCCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 AGGCCGGCTCGGAGGACGACGCGCGACGCTGAGCCCGCAGCTGAGCCCGCACATCTCCCCGGTC 193

Qy    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db    194 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCTTGGTGGGCAACTCGCTGGTC 253

Qy    241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTACATATTTAAC 313

Qy    301 CTGGCTTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 CTGGCTTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTG 373

Qy    361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ATGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 433

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG 493

Qy    481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 553

Qy    541 TGCATCTCGGCTGCTGCGTCTGTCGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 TGCATCTCGGCTGCTGCGTCTGTCGTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAA 613

Qy    601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 GTCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCC 673

Qy    661 TGGTGGGACCTCCTTCATGAAGATCTGCGTCTTCGCCTTCGTGATCTTTCGTGATCCCGTGCTCTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 TGGTGGGACCTCCTTCATGAAGATCTGCGTCTTCGCCTTCGTGATCTTTCGTGATCCCGTGCTCTC 733

Qy    721 ATCATCATCGTCTGCTACACCCCTGATCGTCGTGATCAATCCTGCAAGAGCGTCCGGCTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 ATCATCATCGTCTGCTACACCCCTGATCGTCGTGATCAATCCTGCAAGAGCGTCCGGCTC 793

Qy    781 GGCTCCCAGAGAAAGATCGCAACCTGCTAGGATCACCAGGATCACCGGTCCTGGTGGTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 GGCTCCCAGAGAAAGATCGCAACCTGCTAGGATCACCAGGATCACCGGTCCTGGTGGTGGTG 853

Qy    841 GCAGTTCGTCTGCTGCGACTCCCATTCATCCTGTGGTGGAGAGCTCTCGGGG 900
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Db    854 GCGGTTTTCGTCTGCTGCGACTCCCATTCATCCTGTGGTGGAGAGCTCTCGGGG 913

Qy    901 AGCACCTCCCACAGCACAGCGTGAATCCCATTCCTGCTATTACTTGCCTTAGCCTAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AGCACCTCCCACAGCACAGCGTGAATCCCATTCCTGCTATTACTTGCCTTAGCCTAT 973

Qy    961 ACCAACAGTAGCCTGAATCCCATTCCTTCTTCTCTACGCCTTTCTGATGAAAATTCAAGCCGGTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 ACCAACAGTAGCCTGAATCCCATTCCTTCTTCTCTACGCCTTTCTGATGAAAATTCAAGCCGGTGT 1033

Qy   1021 TTCCGGGACTTCTCGTTCTCGCTTCTCCACTGAAGATGAGGATGAGGCGGCGCACTAGCAGAGTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 TTCCGGGACTTCTCGTTCTCGCTTCTCCACTGAAGATGAGGATGAGGCGGCGCACTAGCAGAGTC 1093

Qy   1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAGTA 1153

Qy   1141 TGACTAGTCGTGGA 1154
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Db   1154 TGACTAGTCGTGGA 1167
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RESULT 14
US-10-318-661-1

; Sequence 1, Application US/10318661
; Publication No. US2003016476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-318-661-1

Query Match   98.9%; Score 1141.4; DB 16; Length 1143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Qy      1 ATGGACTCCCGATCCCAGATCTTCCGCGGGGAGGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
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Db      1 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGGCCGGGCCCTACCTGCGCCCCGAGCGCC 60

Qy     61 TGCCTGCCCCCAACAGCAGCAGCGCGCGGCTGGTTCCCGGTCGGCCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTGCCCCCAACAGCAGCAGCGCGCGGCTGGTTCCCGGTCGGCCCGACAGCAACGGC 120

Qy    121 AGGCCGGCTCGGAGGACGGCGCAGCTGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGCCGGCTCGGAGGACGGCGCAGCTGAGCCCGCACATCTCCCCGGCCATCCCGGTC 180

Qy    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCTTGGTGGGCAACTCGCTGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCATCACGGCCGGTCTACTCCGTAGTGTTCGTCGTGGCTTGGTGGGCTTGGTGGGCAACTCGCTGGTC 240

Qy    241 ATGTTCGTGATCATCCGATACAACAACCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGTTCGTGATCATCCGATACAACAACCAACCAACATTTACATATTTAAC 300

Qy    301 CTGGCTTTTGGGGATGTGCTTAGTGCTCCTTGCGTCTTCATCTTGCGTCTTCATCTTTCGTCGTCCCTGCTCCTC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGCTTTTGGGGATGTGCTTAGTGCTCCTTGCGTCTTCATCTTGCGTCTTCATCTTTCGTCGTCCCTGCTCCTC 360

Qy    361 ATGAATTCCTGGGCCTTTGGGGATGTGCTGCAAGATTTCAAGGCGTGT 420
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Db    361 ATGAATTCCTGGGCCTTTGGGGATGTGCTGCAAGATTTCAAGGCGTGT 420

Qy    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTGACACCGTG 480
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Db    421 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGTGACACCGTG 480

Qy    481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCCACCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATC 540
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Query Match   98.5%;   Score 1136.2;   DB 16;   Length 1284;
Best Local Similarity 99.7%;   Pred. No. 0;
Matches 1138;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy      2  TGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCCT   61
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Db    113  TCGACTCCCGATCCAGATCTTCCGCGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCCT  172

Qy     62  GCCTGCCCCCAACAGCAGCGCCGGCCTGGGCCGAGCCCGACAGCAACGGCA  121
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Db    173  GCCTGCCCCCAACAGCAGCGCCGGCCTGGGCCGAGCCCGACAGCAACGGCA  232

Qy    122  GCGCCGGCTCGGAGACGCGCAGTCGGAGCCGCGCACATCCCCGGCCATCCCCGGTCA  181
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Db    233  GCGCCGGCTCGGAGACGCGCAGTCGGAGCCGCGCACATCCCCGGCCATCCCCGGTCA  292

Qy    182  TCATCACGCGGGTCTACTCCGTAGTGTTCGTCGTGGCCTTGGTCGTCGTGGTG  241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293  TCATCACGCGGGTCTACTCCGTAGTGTTCGTCGTGGCCTTGGTCGTCGTGGTG  352

Qy    242  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC  301
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Db    353  TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACC  412

Qy    302  TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGTACGGTCTACTTGA  361
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Db    413  TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGATGTACGGTCTACTTGA  472

Qy    362  TGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA  421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    473  TGAATTCCTGGCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTACA  532

Qy    422  ACATGTTCACCAGCATCTTCACCTTGACTTCCGCACACCCTGAGGCAAAGATCATCAATATCT  481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533  ACATGTTCACCAGCATCTTCACCTTGACTTCCGCACACCCTGAGGCAAAGATCATCAATATCT  592

Qy    482  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAGGCAAAGATCATCAATATCT  541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593  GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTGAGGCAAAGATCATCAATATCT  652

Qy    542  GCATCTGCGTGCTGTCGTCGTCATCGTGTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  601
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653  GCATCTGCGTGCTGTCGTCGTCATCGTGTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  712

Qy    602  TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCT  661
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Db    713  TCAGGGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCTCA  772

Qy    662  GGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTCA  721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773  GGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCCCGTCCTCA  832

Qy    722  TCATCATCGTCTGCTACACCCTGACTGCGTCTCAAGAGCGTCCGGCGTCCTTTCTG  781
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Db    833  TCATCATCGTCTGCTACACCCTGACTGCGTCTCAAGAGCGTCCGGCGTCCTTTCTG  892

Qy    782  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTCGTGG  841
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893  GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCCACCAGACTGGTCCTGGTCGTGTGG  952

Qy    842  CAGTCTTCGTCGTCTGGACTCCATTCACATATTCATCCTGGTGGAGAGGCTCTGGGGA  901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953  CAGTCTTCGTCGTCTGGACTCCATTCACATATTCATCCTGGTGGAGAGGCTCTGGGGA  1012

Qy    902  GCACCCCCACGACAGCAGTTGCTCTCCAGCTATTACTTCGCATCGCCTTAGGCTATA  961
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Db   1013  GCACCTCCCACGACAGCAGTTGCTCTCCAGCTATTACTTCGCATCGCCTTAGGCTATA  1072

Qy    962  CCAACAGTAGCCTGAATCCATTCTCTTACGGCCTTTCTTGATGAAATTTCAAGCGGTGTT  1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073  CCAACAGTAGCCTGAATCCCATTCTCTACGGCCTTTCTTGATGAAACTTCAAGCGGTGTT  1132

Qy   1141  TGA  1143
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Db   1141  TGA  1143
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RESULT 15
US-10-318-661-3
; Sequence 3, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
US-10-318-661-3

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Qy  1022 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCGAGAGCACTAGCAGAGTCC 1081
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Db  1133 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCGAGAGCACTAGCAGAGTCC 1192

Qy  1082 GAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTAT 1141
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Db  1193 GAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAGTAG 1252

Qy  1142 G 1142
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Db  1253 G 1253
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Search completed: April 6, 2005, 13:18:10
Job time : 769.333 secs

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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    April  6, 2005, 12:28:42 ; Search time 4384.33 Seconds
                                       (without alignments)
                                       10018.893 Million cell updates/sec

Title:          US-09-904-584-4
Perfect score:  1154
Sequence:       1 atggactcccgatccagat.........ccagtatgactagtcgtgga 1154
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched:       34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	805.2	69.8	895	6	CB565888	CB565888 AGENCOURT
2	581.8	50.4	762	7	CO960667	CO960667 AGENCOURT
c 3	518.8	45.0	784	7	CO960682	CO960682 AGENCOURT
4	470.6	40.8	837	7	CF593603	CF593603 AGENCOURT
5	466.4	40.4	480	5	BX092912	BX092912 BX092912
6	429.2	37.2	2405	2	AK038389	AK038389 Mus muscu
7	418.4	36.3	4022	3	AK043873	AK043873 Mus muscu
8	366.2	31.7	2919	3	AK038620	AK038620 Mus muscu
9	366.2	31.7	2959	3	AK079529	AK079529 Mus muscu
10	350.4	30.4	879	3	AY410745	AY410745 Homo sapi
11	334	28.9	2940	3	AK044178	AK044178 Mus muscu
12	325.8	28.2	2974	3	AK043275	AK043275 Mus muscu
13	325.4	28.2	3101	3	AK031926	AK031926 Mus muscu
14	324.2	28.1	879	9	AY410747	AY410747 Mus muscu
c 15	309.8	26.8	1053	5	CNS04C2T	CNS04C2T Tetraodon
16	277.6	24.1	775	5	BX874804	BX874804 BX874804
17	274.2	23.8	787	7	CN439929	CN439929 BB04021A1
18	270.2	23.4	917	5	BU219878	BU219878 603749479
19	269.8	23.4	888	2	BF676176	BF676176 602084171
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22	239.8	20.8	657	2	BB588668	BB588668 BB588668
23	229.6	19.9	682	9	AY410746	AY410746 Pan trogl
24	228	19.8	1176	9	AY400827	AY400827 Homo sapi
25	227.4	19.7	389	2	BE649947	BE649947 UI-M-BH3-
26	225	19.5	1176	9	AY400829	AY400829 Mus muscu
27	225	19.5	2014	9	AK046464	AK046464 Mus muscu
28	224.6	19.5	980	4	BM543468	BM543468 AGENCOURT
29	223	19.3	632	8	BB641725	BB641725 BB641725
30	219.8	19.0	1006	9	AY400676	AY400676 Mus muscu
31	216	18.7	784	5	BQ179053	BQ179053 UI-M-EV0-
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34	213.2	18.5	1006	9	AY400674	AY400674 Homo sapi
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36	213	18.5	836	9	CNS02261	CNS02261 Tetraodon
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45	203.4	17.6	785	4	BI754749	BI754749 60302546S

ALIGNMENTS

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RESULT 1
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LOCUS       CB565888                895 bp    mRNA    linear   EST 02-APR-2003
DEFINITION  AGENCOURT 12691503 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:6519213 5', mRNA sequence.
ACCESSION   CB565888
VERSION     CB565888.1  GI:29485418
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Guthrie cDNA Resource Center
            cDNA Library Preparation: Guthrie cDNA Resource Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBF001 row: f  column: 09
            High quality sequence stop: 763.
FEATURES             Location/Qualifiers
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                     /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA).
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.preSV.dat
                     a. Note: this is a NIH_MGC Library."
ORIGIN
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 762)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Guthrie cDNA Resource Center
                cDNA Library Preparation: Guthrie cDNA Resource Center
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: IRB18   row: d   column: 04
                High quality sequence start: 30
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                     /mol_type="mRNA"
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                     /clone="IMAGE:7389810"
                     /tissue_type="mixed"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_146"
                     /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.presV.dat
                     a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match   50.4%; Score 581.8; DB 7; Length 762;
Best Local Similarity   97.1%; Pred. No. 1.2e-141;
Matches   603; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy   1 ATGGACTCCCGATCCAGATCTTCGGCGGGAGCCGGGCCCTACCTGCGCCCGAGCGCC 60
            ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   27 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 86

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAGCAACGGC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAGCAACGGC 146

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCCACATCTCCCCGGCCATCCCGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCCACATCTCCCCGGCCATCCCGGTC 206

Qy   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCAACTCGCTGGTC 266

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
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Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 386

Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 420
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(second alignment block, left portion)

Query Match   69.8%; Score 805.2; DB 6; Length 895;
Best Local Similarity   97.1%; Pred. No. 2.1e-200;
Matches   841; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

Qy   1 ATGGACTCCCGATCCAGATCTTCGGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 60
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Db   2 ATGGAATCCCGATTCAGATCTTCCGCGGGGAGCCGGGCCCTACCTGCGCCCCGAGCGCC 61

Qy   61 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAGCAACGGC 120
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Db   62 TGCCTGCCCCCAACAGCAGCGCCTGGTTCCCGGCCGGAGCCCGACAGCAGCAACGGC 121

Qy   121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCCACATCTCCCCGGCCATCCCGGTC 180
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Qy   181 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
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Db   182 ATCATCACGGCGGTCACTCCGTAGTGTTCGTCGTGGGCTTGGTGGCAACTCGCTGGTC 241

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Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
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Qy   361 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 420
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Db   362 ATGAATTCCTGGCCTTTGGGGATGTGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 421

Qy   421 AACATGTTCACCAGCATCTCACCTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG 480
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Db   422 AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGGCGTGGACCGCTACATTGCCGTG 481

Qy   481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACCCACACCCACACCCACGATCATCAATATC 540
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Db   482 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACCCACACCCACGATCATCAATATC 541

Qy   541 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 TGCATCTGGCTGCTGTCGTCGTCATCTGTTGGCATCTCTGCAATAGTCCTTGAGGCACCAAA 601

Qy   601 GTCAGGGAAGACGTCGATGTCATTGAGTGCTGCTTCCTTGCAGTTCCCAGATGACTACTCC 660
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Qy   661 TGGTGGGACCTTCTCATGAAGATCGCGTCTTCATCTTTGCCTTCCGTGATCCCGTCCTC 720
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Db   662 TGGTGGGACCTTCTCATGAAGATCGCGTCTTCATCTTTGCCTTCCGTGATCCCGTCCTC 721

Qy   721 ATCATCATCGTCTGTACACCCTGATGATCCGCTGCGTCTCAAGAGCGTCC-GGCTCCTTTC 779
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Qy   780 TGGCTCCCGAGAGAAAGATC-GCAACCTGCGTAGGATCACCAGACTGGTTCCTGGTGGTGG 838
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Db   782 TGGCTCCCGAGAGAAAGATCNGCACCCTGCGTAGGATCACCAGACTGGTTCCTGGTGGTGG 841

Qy   839 TGGCAGTCTTCGTCGTCTGCTGGACT 864
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Db   842 GTGGGCCAGGTCTTCGTCGTCCGTCTGGCT 867

RESULT 2
CO960667
LOCUS   CO960667   762 bp   mRNA   linear   EST 17-AUG-2004
DEFINITION AGENCOURT 30842630 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:7389810 5', mRNA sequence.
ACCESSION   CO960667
VERSION   CO960667.1 GI:5135223
KEYWORDS   EST.

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Db    387  ATGAATTCCTGGCCTTTTGGGATGGTCGCTGTGGCAAGATAGTAATTTCCATTGATTACTAC  446

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Db    447  AACATGTTCACCAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTG     506

Qy    481  TGCCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAACGGCAAAGATCATCAATATC  540
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Db    507  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCTTGAACGGCAAAGATCATCAATATC  566

Qy    541  TGCATCTGGCT-GCTGTCGTCATCGTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAA   599
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Db    567  TGCATCTGGCTGGCTGTCGTCATCGTGTGGCATCTCTGTTAGCATCTCTGCTATAATCCTTGGGGAGGCGCAA  626

Qy    600  AGTCAGGGAAGAGACTCGATGT     620
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Db    627  AATCAGGGAAGAGACTCGAAGGT  647

RESULT 3
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LOCUS       CO960682                 784 bp    mRNA    linear   EST 17-AUG-2004
DEFINITION  AGENCOURT_30842262 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:7389810 3', mRNA sequence.
ACCESSION   CO960682
VERSION     CO960682.1  GI:51125238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 784)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Guthrie cDNA Resource Center
            cDNA Library Preparation: Guthrie cDNA Resource Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBI8  row: d   column: 04
            High quality sequence start: 214
            High quality sequence stop: 494.
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                     /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                     multiple; ORF's were PCR-amplified (from IMAGE clones or
                     from commercially available cDNA libraries) and cloned by
                     the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                     into pcDNA3.1. For specific information on cloning sites
                     (which vary by clone), please refer to the Guthrie
                     website, using the Guthrie ID given in the file
                     ftp://image.llnl.gov.image.rearrayed_plates/IRBF.presv.dat
                     a. Note: this is a NIH_MGC Library."
ORIGIN
Query Match    45.0%;  Score 518.8;  DB 7;   Length 784;
Best Local Similarity  97.6%;  Pred. No. 4.3e-125;
Matches 537;  Conservative  0;  Mismatches  12;  Indels  12;  Gaps  1;
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Db    577  CCTTGGAGGCACCAAAGTCA-GGAAGACGTCGATGTCATTGAGTGCTCCTTGCAGTTCCCA  519

Qy    646  GATGATGACTACTCCTGGTGGGGACCTTCTTCATGAAGATCGCGTCTTCTTTGCCTTC  705
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Db    518  GATGATGACTACTCCTGGTGGGGACCTTCTTCATGAAGATCGCGTCTTCATCTTTGCCTTC  459

Qy    706  GTGATCCTGTCCTCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCCAAGAGC  765
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Qy    766  GTCCGGCTCCTTTCTGGCTCCCGGAGAGAAAGATCGCAACCTGCGTAGGACTACCAGACTG  825
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Qy    826  GTCCTGGTGGTGGTGGTGGCAGTCTTCGTCGTCTGCGTCTGGACTCCCATTCACATATTCACATATTCCTG  885
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Db    338  GTCCTGGTGGTGGTGGTGGCAGTCTTCGTCGTCTGCGTCTGGACTCCCATTCACATATTCACATATTCCTG  279

Qy    886  GTGGAGGCTCTGGGGAGCACCTCCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGC  945
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Qy    946  ATCGCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCTCACGCCTTTCTTGATGAA  1005
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Db    218  ATCGCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTTTTACGCCTTTCTTGATGAA  159

Qy   1006  AATTTCAAGCGGTGTTTCCGGGACTTCGCTTTCCACTGAAGATGAGGAGGGCAG  1065
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Db    158  GACTTCAAGCGGTGTTTCCGGGACTTCGCTTTCCACTGAAGATGAGGAGGGCAG  99

Qy   1066  AGCACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGG  1125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98  AGCACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGG  39

Qy   1126  ATGAATAAAC  1135
           |||  ||||
Db     38  ATGATGAACC  29

RESULT 4
CF593603
LOCUS       CF593603                 837 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  AGENCOURT_15623822 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30531690 5', mRNA sequence.
ACCESSION   CF593603
VERSION     CF593603.1  GI:36347316
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 837)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM622  row: n  column: 19
            High quality sequence stop: 592.
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FEATURES
source   Location/Qualifiers
                1. .837
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3051690"
                /tissue_type="Human Placenta"
                /lab_host="DH10B TonA"
                /clone_lib="NIH_MGC_147"
                /note="Organ: placenta; Vector: pBluescriptR; Site 1:
                all-XhoI; Site_2: BamHI; Oligo-dT primed using primer
                5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                insert size 2.3 kb and normalized to ROT 5. This is a
                primary library enriched for full-length clones and
                constructed using the Cap-trapper method (Carninci, in
                preparation). Library constructed by M. Brownstein
                (NIMH/NHGRI, National Institutes of Health). Note: This is
                a NIH_MGC library."

ORIGIN

Query Match   40.8%;   Score 470.6;   DB 7;   Length 837;
Best Local Similarity 99.2%;   Pred. No. 2.1e-112;
Matches 473;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

Qy   1 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCGAGCGCC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCCGGCCCTACCTGCGCCCGAGCGCC 299

Qy   61 TGCCTGCCCCCACACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 TGCCTGCCCCCACACAGCAGCAGCGCCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGC 359

Qy   121 AGCGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGCGCCACATCTCCCCGGCCATCCGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 AGCGCCGGCTCGGAGGACGGCCAGCTGGAGCCCGCGCCACATCTCCCCGGCCATCCGGTC 419

Qy   181 ATCATCACGGGGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGCTGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 ATCATCACGGGGGTCTACTCCGTAGTGTTCGTCGTGGGGCTTGGTGGGCAACTCGCTGGTC 479

Qy   241 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 ATGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 539

Qy   301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTG 599

Qy   361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 ATGAATTCCTGGCCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 659

Qy   421 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGGTGGACCATTGCC 477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 AACATGTTCACCAGACATCTTCACCTTGACCATGATGAGCGTGGACCGGTGGACCATTGCC 716

RESULT 5
LOCUS   BX092912   480 bp   mRNA   linear   EST   23-JAN-2003
DEFINITION   BX092912 Soares placenta Nb2HP Homo sapiens cDNA clone
                IMAGp998B19190 ; IMAGE:134322, mRNA sequence.
ACCESSION   BX092912
VERSION   BX092912.1 GI:27823005
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 480)
AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
                Radelof,U., Schneider,D. and Korn,B.
TITLE   Human UnigeneSet - RZPD3

JOURNAL   Unpublished (2003)
COMMENT   Contact: Ina Rolfs
                RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                RZPD; IMAGp998B19190.
                RZPDLIB, I.M.A.G.E. cDNA Clone Collection;
                Human UnigeneSet - RZPD3 (RZPDLIB No.972)
                http://www.rzpd.de/CloneCards/cgi-
                bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
                RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                Heubnerweg 6, D-14059 Berlin, Germany
                Tel: +49 30 32639 101
                Fax: +49 30 32639 111
                www.rzpd.de
                This clone is available royalty-free from RZPD;
                contact RZPD (clone@rzpd.de) for further information. Seq primer:
                M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

FEATURES
source   Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGp998B19190 ; IMAGE:134322"
                /sex="Female"
                /dev_stage="placenta obtained at birth (full term)"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares placenta Nb2HP"
                /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                AACTGGAAGAATCGGCGCAGGAATTTTTTTTTTTTTTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match   40.4%;   Score 466.4;   DB 5;   Length 480;
Best Local Similarity 99.8%;   Pred. No. 2.3e-111;
Matches 467;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy   687 CGTCTTCATCTTGCCTTCGTGATCCCTGTCCTCATCATCGTCTGCTACACCCTGAT 746
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Db   1 CGTCTTCATCTTGCCTTCGTGATCCCTGTCCTCATCATCGTCTGCTACACCCTGAT   60

Qy   747 GATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGCTCCCGAGAGAAAGATCGCAACCT 806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGCTCCCGAGAGAAAGATCGCAACCT 120

Qy   807 GCGTAGGATCACCAGACTGGTCCTGGTGGTGGGCTCGTGGGAGGCTCGTCGTCTGGGACTCC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCGTAGGATCACCAGACTGGTCCTGGTGGTGGGCTCGTGGGAGGCTCGTCGTCTGGGACTCC 180

Qy   867 CATTCACATATTCATCCTGTGGGAGGCTCTGGGAGGCACCTCCCACAGTAGCCTGATCCTGAATCCCATTCT 926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CATTCACATATTCATCCTGTGGGAGGCTCTGGGAGGCACCTCCCACAGTAGCCTGATCCTGAATCCCATTCT 240

Qy   927 CTCCAGCTATTACTTCTGCGATCCGCTTAGGCTATACCAACAGTAGCCTGAATCCCACTGA 986
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Db   241 CTCCAGCTATTACTTCTGCGATCCGCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCT 300

Qy   987 CTACGCCTTTCTTGATGAAAATTTCAAGCAGCTTCGTTCCGGGACTTCTGCTTCTGCCACTCGAA 1046
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Db   301 CTACGCCTTTCTTGATGAAAATTTCAAGCAGCTTCGTTCCGGGACTTCTGCTTCTGCCACTCGAA   360

Qy   1047 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA 1106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GATGAGGATGGAGCGGCAGAGCACTAGCACAGTCCGAAATACAGTTCAGGATCCTGCTTA 420

Qy   1107 CCTGAGGGACATCGATGGGATGAATGAATAAACCAGTAGTCGTCGTGA 1154
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Db   421 CCTGAGGGACATCGATGGGATGAATGAATAAACCAGTAGTCGTCGTGA 468

```
RESULT 6
AK038389
LOCUS       AK038389              2405 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230002D02 product:opioid receptor, mu,
            full insert sequence.
ACCESSION   AK038389
VERSION     AK038389.1  GI:26332528
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2405)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,Y., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,H., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1..2405
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A230002D02"
                     /db_xref="taxon:10090"
                     /clone="A230002D02"
                     /sex="male"
                     /tissue_type="hypothalamus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             41..1357
                     /note="unnamed protein product; opioid receptor, mu
                     (MGD|MGI:97441, GB|NM_011013, evidence: BLASTN, 99%,
                     match=1197)
                     putative"
                     /codon_start=1
                     /proteIn_id="BAC29982.1"
                     /db_xref="GI:26332529"
                     /translation="MDSSAGPGNISDCSDPLAPASCSPAPGSWLNLSHVDGNQSDPCG
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                     MSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCT
                     LTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLR
                     RITRMVLVVVAVFIVCWTPIHIYVIIKALITIPETFQTVSWHFCIALGYTNSCLNPV
                     LYAFLDENFKRCFREFCIPTSSTIEQQNSARIRQNTREHPSTANTVDRTNHQPTLAVS
                     VAQIFTGYPSPTHVEKPCKSCMDRGMRNLLPDDGPRQESGEGQLGR"
ORIGIN
Query Match            37.2%;    Score 429.2;   DB 3;    Length 2405;
Best Local Similarity  65.6%;    Pred. No. 2.1e-101;
Matches  661;  Conservative    0;  Mismatches 338;  Indels    9;  Gaps    2;

Qy         92 CCGGCTGGCCGAGCCCGACAGCAACGGCAGCGCCGGCTCGGAGGACCGCAGCTGGAGC 151
              ||| |||||| |||||||||| ||||| |||||| ||||||| ||| ||| || ||||
Db        159 CCGACCCATGCGGTCCTAACCGACGCGGGCTTGGCGGGGAGCCACAGCCTGTGCCCTCAGA 218

Qy        152 CCGCGCACATCTCCCCGGCCCATCCGGTCATCATCACGGCGGTCTACTCCGTAGTGTTCG 211
              || |||| ||| ||||| ||||||||  |||||||||| ||||||| ||| || | | |
Db        219 CAGCAGCCCTTCCATGGTCAGAGCCATCACCATCATGCGCCCTCTATTCTATCGTGTGTG 278

Qy        212 TCGTGGGCTTGGTGGGCAACTCCGTGGTCATGTTCGTGATCATCCGATCACAAAGATGA 271
              | ||||||||||||| |||||||||||  ||||||||||  |||||| ||||   |||
Db        279 TAGTGGGCCTCTTTGGAAACTTCCTGGTCATGTATGTGATTGATTGTAAAGATATACCAAAAATGA 338

Qy        272 AGACAGCAACCAACATTTACATATTTAACCTGGCTTTGCAGATGCTTTAGTTACTACAA 331
              |||||||||||||||| ||||  |||||||||| ||  |||| |  || |||| ||| |
Db        339 AGACTGCCACCAACATCTACATTTTCAACCTGTCTCGGCCAGATGCCTTAGCCACTAGCA 398

Qy        332 CCATGCCCTTTCGAGAGTACGGTCTACTTGATGAATTCCTGGGCTTTTGGGGATGTCGTGT 391
              |||||||||||||||||    ||| ||||||||||||  |||||  ||||| ||||| |
Db        399 CGCTGCCCTTTCCAGAGTTGTTAACTCACCTGATGGGAACGTGGCCCTTTGGAAACATCCTCT 458

Qy        392 GCAAGATAGTAATTCCATTGATTACTACAACATGTTCACCTTGACCA 451
              |||||| |||  |||||||||| |||| |||| ||| ||||||||| |
Db        459 GCAAGATCGTGATCTCAATAGACTACTACAACATGTTCACCAGTATCTTCACCCTCTGCA 518

Qy        452 TGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCGTGAGGGCTTTGGACTTCCGCA 511
              |||| | || |||  |||| | |||||| ||||||||  |  |||  |||| || |||
Db        519 CCATGAGTGTAGACCGCTACATTGCCGTCGCGCCACCCGTCAAGGCCCTGGATTTCCGTA 578

Qy        512 CACCCTTGAAGGCAAAGATCATCAATATCGATCTCGGCTGCTCGTCGTCGTTGGCA 571
              ||  |  |   ||||| ||   | ||||| ||| | ||| | ||||  |||| ||||
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Db   579  CCCCCGAAATGCCAAAATTGTCAATGCTGCAACTGGATCCTCCTTCCTCTGCCATTGGTC  638
                |||| | | |||   ||||||  || ||||| ||| |||  |||  ||| |||||
Qy   572  TCTCTGCAATAGTCCTTGGAGGCCACCAAAGTCAGGGAAGACGTCGATGTCATTGAGTGCT  631
                |  |||| ||  ||||    ||||    | |||      |||    |||
Db   639  TGCCCGTAATGTTCATGGCAACCACAAAATACAGGCAGGGGTC------CATAGATTGCA  692

Qy   632  CCTTGCAGTTCCCAGATGATGACTACTCCTCGTGGGACCTCTTCATGAAGATCTCGCTCT  691
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Db   693  CCCTCAGTTCTCTCATCCCACATGGTACTGGGAGAACCTGCTC---AAAATCTGTGTCT  749

Qy   692  TCATCTTTGCCTTCGTGATCCCTGATCCTCATCATCATCGTCTGCTACACCCTGATGATCC  751
                |||||| | ||||  |  |||| |||| ||||| |||||||| ||||| |||||
Db   750  TCATCTTCGCCTTCATCATCGCCGGTCCTCATCATCACTGTGTGTTATGGACTGATGATCT  809

Qy   752  TGCGTCTCAAGAGAGGCTCCGGCTCCTTCTTCGGCTCCCGAGAGAAAGATCCGCAACCTGCGTA  811
                ||| ||||||||       |||||  ||| | |||||||||| ||||||||||| |||||
Db   810  TACGACTCAAGAGTGTCCGCATGCTGTCCGGCTCCAAAGAAAAGGACACAGGAACCTGCGCA  869

Qy   812  GGATCACCAGACTGGTCCTGGTGGTGGCAGTCTTCGTCGTCTGGACTCCCATTC  871
                ||||||| || | |||||| || | | |||| ||  ||||| ||| ||||
Db   870  GGATCACCCGGATGGTGCTGGTGCTGGTGGTCGTGGTGGCTGTATTGTCTGGACCCCATCC  929

Qy   872  ACATATTCATCCTGGTGGAGGCTTCTGGGAGGCACCTCCCACAGCACAGTCGCTCTCCA  931
                || ||||||| | |  | ||||||||  |  | || |  || |||||| ||| |||||
Db   930  ACATCTATGTCATCATCAAAGCACTGATCATCAACCCACTTTCCAGACTGTTT  989

Qy   932  GCTATTACTTCTGCATCGCCTTAGGCTATCATACCAACCAGTAGCCTGAATCCCCATTCCTCTACG  991
                || |||||  |||||| ||||| | || |  | | | |  || |||| ||||||| | |
Db   990  CCTGGCACTTCTGCATTGCCTTCGGTTACGTGAACAGCTGCCTGAACCCAGTTCTTTATG  1049

Qy   992  CCTTTCTGATGAAAATTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGA  1051
                || |||||||||| ||||    ||| ||| ||| |   |||| |  |||  ||
Db   1050 CGTTCCTGATGAAGAACTTCAAACGATGTTTAGAGAGTTTCGCATCCCAACTTCCTCCA  1109

Qy   1052 GGATGGAGCGGCAGAGCACTAGCAGAGTCCGAAATACAGTTCAGGATC  1099
                || ||||| | ||  |  | |  || || | |||||| |||||||
Db   1110 CAATCGAACAGCAAAACTCTGCTGAATCCGTCAAAACACTAGGGAAC  1157
```

RESULT 7
AK043873

LOCUS   AK043873   4022 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830044L10 product:DELTA-TYPE OPIOID
            RECEPTOR, full insert sequence.
ACCESSION   AK043873
VERSION   AK043873.1 GI:26335979
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE 99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE 20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akimura,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,A.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

TITLE   Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE 20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4022)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,J., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
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RESULT 8
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DEFINITION   Mus musculus adult male hypothalamus cDNA, RIKEN full-length
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               (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK038620
VERSION   AK038620.1 GI:26332698
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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  TITLE   RIKEN integrated sequence analysis (RISA) system-384-format
               sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
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REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
               FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2919)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
               Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
               Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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               Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,
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               Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
               Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
               Physical and Chemical Research (RIKEN), Laboratory for Genome
               Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
               RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
               Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
               URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
               Fax:81-45-503-9216)

ORIGIN

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DEFINITION     Mus musculus adult male hypothalamus cDNA, RIKEN full-length
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               (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION      AK079529
VERSION        AK079529.1  GI:26348047
KEYWORDS       HTC; CAP trapper.
SOURCE         Mus musculus (house mouse)
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               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1
  AUTHORS      Carninci,P. and Hayashizaki,Y.
  TITLE        High-efficiency full-length cDNA cloning
  JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE      99279253
   PUBMED      10349636
REFERENCE      2
  AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE      20499374
   PUBMED      11042159
REFERENCE      3
  AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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  TITLE        RIKEN integrated sequence analysis (RISA) system--384-format
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COMMENT        cDNA library was prepared and sequenced in Mouse Genome
               Encyclopedia Project of Genome Exploration Research Group in Riken
               Genomic Sciences Center and Genome Science Laboratory in RIKEN.
               Division of Experimental Animal Research in Riken contributed to
               prepare mouse tissues.
               Please visit our web site for further details.
               URL:http://genome.gsc.riken.jp/.
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FEATURES             Location/Qualifiers
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JOURNAL      sequencing pipeline with 384 multicapillary sequencer
             Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED       11076861
REFERENCE    4
AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
TITLE        Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409, 685-690 (2001)
REFERENCE    5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE        Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    6  (bases 1 to 2959)
AUTHORS      Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Yoshihide Hayashizaki (RIKEN), The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
             URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.jp/
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                     FSFIIPVLIISVCYSLMIRRLRGVRLLSGSREKDRNLRRITRLVLVVVAVFVGCWTPV
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     polyA_signal    2939..2944
                     /note="putative"
     polyA_site      2959
                     /note="putative"

ORIGIN

Query Match             31.7%;    Score 366.2;  DB 3;  Length 2959;
Best Local Similarity   63.3%;    Pred. No. 8.1e-85;
Matches   598;  Conservative   0;  Mismatches  338;  Indels   9;  Gaps    2;

Qy    154 GCGGACAATCTCCCCGGCCATCCCCGGTCATCATCACGGCGGTCTACTCCGTAGTGTTCGTC 213
          ||||||    |||   ||||||    |||  ||||| ||||||| |||||||||| |||||
Db    341 GCCTTCCTGCCCCTTGGACTCAAGGTCAAGGTCACCATCGTGGGGCTCTACTTGGCTGTGCATC 400

Qy    214 GTTGGGCTTGGTGGGCAACTCGCTGGTCATGTTCGTGGTCATCATCCTGGGATCATCGATACAAGATGAAG 273
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Db    401 GGGGGGCTCCTGGGGAACTGGCCTGCTCCTCATGTATGTCATCCTCAGGCACCAAGATGAAG 460

Qy    274 ACAGCAACCAACATTTACATATTTAACCTGGCTTGGAGATGTTTAGTTACTACAACC 333
          ||    || |||||||||||||| |||||| |||||||
Db    461 ACTGCTACCAACATTTACATATTTAATCTGGCACTGGCGCTGGTCTTGCTGACA 520

Qy    334 ATGGCCCTTTCAGATACGGTCTACTTGATGAATTCCTGGCCTTTGGGGATGTGCTGTGC 393
          |||||| ||||| |||||| ||| |||  |||||||| |||| ||||||||||||||
Db    521 CTGCCCTTTCCAGGGCACAGACATCCTTCTGGCCTTTCGGCCATTGGGAATGCACTGTGC 580

Qy    394 AAGATAGTAATTCCATTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATG 453
          |||||    |||| |||||||||||||||||||||||||||||  |||||
Db    581 AAGACGGTCATTGCATTGCTATCGACTACAACATGTTTACCAGCACTTTGACTGCC 640

Qy    454 ATGAAGCGTGACCGCTACATTGCCGTGTCGCACCCCGTGAAGGCTTTGGACTTCCGCACA 513
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Db    641 ATGAGTGTAGACCGTTATGTGAGCTATCTGCCACCCTATCGTGCTCTTGGATGTTCGGACA 700

Qy    514 CCCTTGAAGGCAAAGATCATCATATCTGCATCGGCGTCGTCGTCATCGTGTTGGCATC 573
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Db    701 TCCAGTAAAGCCCAGGCCGTTAATGTGGCCATATGGGCCCTGGCTTCGGTGGTTGGTGTT 760

Qy    574 TCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGAGGACGTCGATGTCATTGAGTGCTCCC 633
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Db    761 CCTGTTGCCATCATGGGGCTCAGCAGCAAGT------GGAGGATGAAGAGATGCCTG 814

Qy    634 TTGCAGTTCCCAGATGATGACTACTCCTGGTGGGACCTTCATGAAGATCTGCGTCTTC 693
          || |||||| |||| |||    |||||    ||||  |||||||||| || ||||||
Db    815 GTGGAGATCCCGCCCCCTCAGGA--CTATTGGGGCCCTGTATTGCCATCTGCATCTTC 871

Qy    694 ATCTTTGCCTTCGTGATCCCTGTCCTCATCATCGTCTGTACACCCTGATGATCCTG 753
          ||||||  |||   |||||||||||    |||||| ||||| ||||||||||||||
Db    872 CTTTTTCCTTCATCATCCCGGTTCTGATCATCTCTGTCTGCTACAGCCTCATGATTCGA 931

Qy    754 CGTCTCAAGAGCGTCCGGCTCCTTCTGGGTGCTGTGGTGTGGGTGTGTGGCTGGAGG 813
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Db    932 CGACTTCGTGGTGTCCGGCTGCTTTCAGGCTCCCGTGAGAAAGGACCGGAACCTGCGACGC 991

Qy    814 ATACCACCAGACTGGTCCTGGTGGTGGCAGTCTTCGTTGGTGCTCCCATTCAC 873
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Db    992 ATCACACGCGCTGGTACTGGTGAGTTGTGGTGGTGGCAGTGTTCGTGGGCTGC 1051

Qy    874 ATATTCATCCTGGGGAGGCTCGGGAGGCTCGGCTCCCCACAGCAGCTGCTCCTCCAGC 933
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Qy    934 TATTACTTCTGCATCGCCGGCTATACCAACAAGAGTCCGAATCCATTCCTTACGCGC 993
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Db    1112 CTGCGCTTCTGCACAGCCCTGGGCTATGTCAATTCCTGTCTCAATCCCATTCTCTATGCT 1171

Qy    994 TTTCTTGATGAAAATTTCAAGGCGTGTTTCCGGACTTCTGTTCCACTGAAGATGAGG 1053
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Db    1172 TTCTTGGATGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTGCTGCGCTTCTGCCCTGCAC 1231

Qy    1054 ATGGAGCCGCAGAGCACTAGCAGAGTCCGAAATACAGTTCAGGAT 1098
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RESULT 10
AY410745
LOCUS   AY410745   879 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Homo sapiens OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY410745
VERSION   AY410745.1 GI:39766713
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 879)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

Query Match   30.4%; Score 350.4; DB 9; Length 879;
Best Local Similarity 65.4%; Pred. No. 8.5e-81;
Matches   548; Conservative 0; Mismatches 281; Indels 9; Gaps 2;

Qy   260 ACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTTAACCTGGCTTGGCAGATGCTT 319
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Qy   320 TAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTG 379
               |||| ||| |||||||| ||||| |||| || || |||| ||||||| | |||
Db   62 TGGTCCTGCTGCACGCTGCCCTTCCAGGGCACGGACCATCCTCCTGGCTTCTGGCCGTTTG 121

Qy   380 GGGATGGTGCTGTGCAAGATAGTAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCT 439
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Db   122 GGAATGCGCTGTGCAAGACAGTCATTGCCATTGACTACTACAACATGTTCACCAGCACCT 181

Qy   440 TCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGGTGCCACCCCGTGAAGGCTT 499
               |||||| ||| |||||||||| || ||||| ||| ||| |||||| ||| ||| ||
Db   182 TCACCCTAACTGCCATGAGTGTGGATCGCTATGTAGCCATCATCCACCCCATCCGTGCCC 241

Qy   500 TGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGCATCTGGCTGTCGTGT 559
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Db   302 CTGTTGTCGCGTGTTCCCGTTCCCATCATGGCCTCGGCACAGGTC-----GAGGATGAAG 355

Qy   620 TCATTGAGTGCTCGTCTTCGACGTTCCCAGATGATGAGCACTCCTGGTGGGACCTCTTCATGA 679
               ||||||||| | ||||| |||| |||||||| ||| |||| ||||| |||||
Db   356 AGATCGAGTGCCTGGTGGCCTGGGAGATCCCTACCCCTCAGGATTAC---TGGGGCCCGGTGTTG 412

RESULT 11
AK044178
LOCUS   AK044178   2940 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830097K10 product:NOCICEPTIN RECEPTOR
            (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK044178
VERSION   AK044178.1 GI:26090219
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection

Qy   680 AGATCTGGTCTTCATCTTCGTCCTGATCCTGGTCCTCATCATCATGCTCTGCTACA 739
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Db   413 CCATCTGCATCTTCCTTCTCTTCATCGTCCTCCTGGTCGTCTCATCTCTGCTCTGCTACA 472

Qy   740 CCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTGGCTCCGAGAGAAGATC 799
               ||| |||||||| ||||||| ||||| |||| |||||| || ||| |||||||| ||||
Db   473 GCCTCATGATCCGGCGCGCTCCGTGAGTCCGCTGCTCCGGCTCCGGCTCCGGAGAAGGAGACC 532

Qy   800 GCAACCTGCGTAGGATCACCAGACTGTCCGTCGTGGTGGTGCAGCTTCGTCGTCGTGCT 859
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Db   533 GGAACCTGCGGCGGCATCACTCGGCTGTGGTGGTGGTGAGTGGCTGTGTTCGTTCGGGGTGCT 592

Qy   860 GGACTCCCATTCACATATTCATCCTGTGGTGGAGGCTCTGGGGAGCCACCTCCCAGACACAG 919
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Db   593 GGAGCGCCTGCTCGTTCGTGCTGCTCCCCAAGGGGCTGGGGGTTCAGCCGAGCAGGCAGGA 652

Qy   920 CTGCTCCTCCAGCTATTACTTCTGATCCATGCCATCGTGCGCCTGGGCTACCAGTAGCCTGAATC 979
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Db   653 CTGCCGGTGGCCATTCTGCTTCTGCGACGGGCCCTGGGCTACGTCACAGCGTGCCTCAACC 712

Qy   980 CCATTCCTACGCCTTTCTTGATGAAAATTCAAGCGGTGTTCCGGGACTTCGCTTTC 1039
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Db   713 CCATCCTCTACGCCTTCCTGATGAGAACTTCAAGGCCCTGCTTCCCGCAAGTTCTGCTGTG 772

Qy   1040 CACTGAAGATGAGGATGGAGCGGCAGCAGAGACCACTAGCAGAGTCCGAAATACAGTTCAGGA 1097
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Db   773 CATCTGCCCCTGCGCCGGGACGTCGACCGGTGTCCGACCGGTGTTCGACCGGAGCATTGCCAAGGA 830

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Qy   315 TGCTTTAGTTAGTACTACAACACATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCTGGCC 374
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Db   543 ATTTGGGGAATGCACTGTGCAAGACGGTCATCTGCTATCGACTACTACAACATGTTTTACCAG 602

Qy   435 CATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCGTGAA 494
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Db   603 CACTTTCACTTTGACTGCCATGAGTGTAGACCGGTTATGTAGCTATCTGCCACCCTATCCG 662

Qy   495 GGCTTTGGACTTCCGCACACCCTGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCT 554
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Db   663 TGCCCCTGATGTTCGGACATCCAGTAAAGCCCAGGCCGTTAATGTGGCCATATGGGCCCT 722

Qy   555 GTCGTCATCTGTTGGCATCTGTCATCATCATGGGCTCAGCACAAGT------GGAGGA 614
         || ||||| || ||||| ||||||  ||  ||||||||||||||||      ||||||
Db   723 GGCTTGGCGGTTGGTGTTCCTGTGCCATCATGGGCTCAGCACACAAGT------GGAGGA 776

Qy   615 CGAATGTCATTGAGTGCTTCCTTGCTCCAGTTCCCAGATGATGACTACTCCTGGTGGGACCTCTT 674
         | ||||||| || |||||| |||  ||||||| ||| ||||||||||  |||| ||||||||
Db   777 TGAAGAGATCGAGTGCCTGGTGGAGATCCCCCTCAGGA---CTATTGGGGCCCTGT 833

Qy   675 CATGAAGAGATCTGCGTCTCATCTTGCCTTCGTGATCCCTGTCCTCATCATCGTCTG 734
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Db   834 ATTTGCCATCGCATCTCGTCATCTTTCCTTTTTCCTTGATCATCCCGGTTCTGATCATCTCTGTCTG 893

Qy   735 CTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCCTCCTTCCTGGCTCTCCCGAGAGA 794
         || ||||||||| ||||||||||| ||||||| ||||| || |||| |||| || ||||||
Db   894 CTACAGCCTCATGATTCACGACTTCGTGTGTCGGCGTTCAGGCTCCCGAGAGAA 953

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Db   954 GGACCGGAACCTGCGGACGCATCACACGGCGTACTGGTAGTTGTGGGCTGTGTTTGTGGG 1013

Qy   855 CTGCTGGACTCCCATTCACATATTCACCTGGTGGAGGCTCTGGGGAGCACCTCCCACAG 914
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Db  1014 CTGCTGGACACCTGGCAGGTCTTTGTCCTGGTTCAAGGACTGGGTGTTCAGCCAGGTAG 1073

Qy   915 CACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGTCTAGGCTCATCGCTATACCACAGTAGCCT 974
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Db  1074 TGAGACTGCAGTAGCCATTCTGCACAGCCCTGGGCTATGTGGTCAACAGTTGTCT 1133

Qy   975 GAATCCATTCTCTACGCCTTCTTGATGAAAATTCAAGCGGTGTGTTTCCGGGACTTCTG 1034
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Db  1134 CAATCCCATTCTCTATGCTTTCTTGGATGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTG 1193

Qy  1035 CTTTCCACTGAAGATGAGGATGGAGCGCGGCAGAGCCTAGCAGAGTCCGAAATACAGTTCA 1094
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Qy  1095 GGAT 1098
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Db  1254 GGAT 1257
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JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
      Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
      of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2940)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
      Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
      Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
      Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
      Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
      Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
      Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
      Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
      Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
      Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
      Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
      Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
      Physical and Chemical Research (RIKEN), Laboratory for Genome
      Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
      RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
      Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
      URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
      Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
      Encyclopedia Project of Genome Exploration Research Group in Riken
      Genomic Sciences Center and Genome Science Laboratory in RIKEN.
      Division of Experimental Animal Research in Riken contributed to
      prepare mouse tissues.
      Please visit our web site for further details.
      URL:http://genome.gsc.riken.jp/
      URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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ORIGIN

RESULT 12
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LOCUS   AK043275   2974 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION   Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
      enriched library, clone:A730079L19 product:NOCICEPTIN RECEPTOR
      (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION   AK043275
VERSION   AK043275.1   GI:26089596
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.

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Query Match             28.9%;  Score 334;  DB 3;  Length 2940;
Best Local Similarity   61.8%;
Matches  596;  Conservative    0;  Mismatches  340;  Indels   28;  Gaps   3;

Qy   154 GCGGACACTCTCCCGGCCATCCGGTCATCATCACGGCGGTCTACTTCGTAGTGTTCGTC 213
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Qy   214 GTGGGCTTGGTGGGCAACTCGCTCGTCGGTCATGTTCGTGATCAT----------- 254
         ||||| ||||  || |||| ||||| || |||||| || || ||
Db   363 GGGGGCTCCTGGGAACTGCCTCGTCGTCATCTGGAGGGCATTGAGGGGAACTGGAGACAG 422

Qy   255 CCGATCACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGCAGA 314
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Db   423 CAGGGCACCAACAGGAAGAGACTGCTACCAACATTTACATATTTAATCGGCACTGGCTGA 482
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TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,A., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2974)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan; (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     match=1135)
                     putative"
     polyA_signal    2951..2956
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     polyA_site      2974
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ORIGIN

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Best Local Similarity   63.3%;  Pred. No. 3.4e-74;
Matches   536; Conservative    0; Mismatches  302; Indels   9;  Gaps    2;

Qy     252 CATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGC 311
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Db     450 CAGCAGGCACCACCAAGATGAAGACTGCTACCAACATTTAACATATTTAATCTGGCACTGGC 509

Qy     312 AGATGCGTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTG 371
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Db     510 TGATACCCTGGTCTTCGCTGCTGCACTGGCCCTTCCAGGGCACAGACATCCTTCTGGGCTTCTG 569

Qy     372 GCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCAC 431
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Db     570 GCCATTTGGGAATGCACTGTGCAAGACGGTCATTGCTATCGACTACTACAACATGTTTAC 629

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Db     630 CAGCACTTTCACTTTGACCTGCCATGAGTGAGACCGTTATGTAGCTATCTGCCACCCTAT 689

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Db     804 GGATGAAGAGATCGAGTGCCTGCCGGTGGTGGAGATCCCGCCCCTCAGGA---CCATTGGGGCCC 860

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Db     921 CTGCTACAGCCTCATGATTCGACGACTTCGTGGTCGTGGTGTTCAGGCTCCCCGAGA 980

Qy     792 GAAAGATCGCAACCTGGTAGGATCACCAGGATCACACAGGCTGGTCGTGGCGTGGCAGTCTTCGT 851
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Db     981 GAAGGACCGAACCTGCGACGCATCACACACGGCTGTACTGGCTAGTGGTGTGGGGCTGTGTTTGT 1040

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Qy    1092 TCAGGAT 1098
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RESULT 13
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LOCUS        AK031926              3101 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION   Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
             enriched library, clone:6330500C19 product:NOCICEPTIN RECEPTOR
             (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION    AK031926
VERSION      AK031926.1  GI:26082601
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
AUTHORS      Carninci,P. and Hayashizaki,Y.
TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
MEDLINE      99279253
PUBMED       10349636
REFERENCE    2
AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE      20499374
PUBMED       11042159
REFERENCE    3
AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE        RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED       11076861
REFERENCE    4
AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
TITLE        Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409, 685-690 (2001)
REFERENCE    5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE        Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    6  (bases 1 to 3101)
AUTHORS      Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
```

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COMMENT      Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
             URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
             cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.jp/.
             URL:http://fantom.gsc.riken.jp/.
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Best Local Similarity   63.3%;     Pred. No. 4.4e-74;
Matches  535;  Conservative   0;  Mismatches 301;  Indels   9;  Gaps    2;

Qy    254 TCGGATCACAAAGATGAAGACAGCAACCAACATTACATATTAACCTGGCTTGGCAG 313
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Db    580 TCAGGCACCAAGATGAAGACTGCTACCAACATTACATATTAACATATTTAATCTGGCACTGGCTG 639

Qy    314 ATGCTTTAGTTACTACAACCATGCCCTTTCAGATGACGGTCTACTTGATGAATTCCTGGC 373
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Qy    614 TCGATGTCATTGAGTGCTGCTCCTTGCAGTTCGCAGTTGACTACTCCTGGTGTGGGACCTCT 673
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Qy    734 GCTACACCCTGATGATCCTGGCTCTCAAGAGAGCGTCCGGCTCCTTCTCGGCTCCCGAGAGA 793
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Qy    320  TAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTG  379
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Qy    380  GGGATGGTGCGTGCAAGATAGTAATTCCATTGATTGATTACAACATGTTCACCAGACATCT  439
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Db    122  GGAATGCACTGTGCAAGACGGTCATTGCTCATGCTACGACTACACAGTGTTACCAGCACTT  181

Qy    440  TCACCTTGACCATGATGAGGCTGGACGCTACATTGCCGTGCCACCCCGTGAAGGCTT  499
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Qy    560  CATCTGTTGGGCATCTCTGCAATAGTCCTTGGAGGGCACCAAAGTCAGGGAGACGTCGATG  619
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Db    356  AGATCCAGTGCGCCTGGTGTGGAGATCCCCCCTCAGA---CTATTGGGGCCCTGTATTTG  412

Qy    680  AGATCTGGCGTCTTCATCTTTGCCTTCGTGATCCCTGTCCTCATCATCATGTCTCTGCTACA  739
           |||| |||||||| || |||||||| ||| ||||| |||||||||||||||||||| ||
Db    413  CCATCTGCATCTTCCTTTTTCCTTCATCATCCCGGTTCTGATCATCTCGTCTGCTGCTACA  472

Qy    740  CCCTGATGATCCTGGGTCTCAAGAGCGTCCGGCTCCTTCTGGCTCCGAGAAGAAGATC  799
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Db    473  GCCTCATGATTCGACGACTTCGTGGTGTGGCCGGCTCCTTCAGGCTCCCCGAGAAGGACC  532

Qy    800  GCAACCTGCGTAGGATCACCAGACTGGTCTGTGGTGGCAGTCTTCGTCGTGCT  859
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Db    533  GGAACCTGCGACGCATCACACGGTACTGGTAGTTGTGGCTGTGTTTGGGCTGCT  592

Qy    860  GGACTCCCATTCACATTCATCCTGGTGGAGGCTTCTGGGAGGCACCTCCCACAGCACAG  919
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Db    593  GGACACCTGTGCAGGTCTTTGTCCTGGTTCCTCAAGGACTGGGGTGTTCAGCCAGTAGTGAGA  652

Qy    920  CTGCTCCTCCAGCTATTACTCTGCCATCCGCCTTAGGCTATGCCAGACTAGCCTGAATC  979
           || | |||||| || ||||||| ||||||||| |||||||||||||||||||||| ||||
Db    653  CTGCAGTAGGCCATTCTGCGCTTCGCACAGCCCTGGGCTATGTCAACAGTTGTCTCAATC  712

Qy    980  CCATTCTCACGCCCTTTCTTGATGAAATTTCAAGCGGCGTGTTCCCGGACTTCTGCTTTC  1039
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Db    713  CCATTCTCATGTCTTTCTTGATGAGAGAACTTCAAGGCCTGCTTTAGAAAGTTCTGCTGTG  772

Qy   1040  CACTGAAGATGAGGATGGACGCGGCAGAGCACTAGCAGAGTTCGAAATACAGTTCAGGAT  1098
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Db    773  CTTCTGCCCTGCACCCGGAGATGCAGGTTTCTGATCGTGTGCGCAGCATTGCCAGGAT  831
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RESULT 14
AY410747

LOCUS   AY410747   879 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Mus musculus OPRL1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY410747
VERSION   AY410747.1 GI:39766715
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 879)
  AUTHORS   Clark,A.G. Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 879)
  AUTHORS   Clark,A.G. Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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Qy    914  GCACAGCTGCTCCTCCAGCTATTACTTCTGCGATCCTGCCTTAGGCTATGCCAGACTAGCC  973
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Db   1171  GCTGCTGGACACCTGTGCAGGTCTTTGTCCTGGTGTTCAAGGACCTGGGTGTTCAGCCAGGTA  1230

Qy    974  TGAATCCCATTCTCACGCCCTTTCTTGATGAAATTTCAAGCCGGTGTTCCCGGGACTTCT  1033
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Db   1231  GTGAGACTGCAGTAGGCCATTCTGCGCTTCGCACAGCCCTGGGCTATGTCAACAGTTGTC  1290

Qy   1034  GCTTTCCACTGAAGATGAGGATGGACGCGGCAGAGCACTAGCAGAGTTCCGAAAATACAGTTC  1093
           |||||| |||||||||||||| |||||| ||||| ||||| | || ||||||
Db   1291  TCAATCCCATTCTCATGTCTTTCTTGGATGAGAGAACTTCAAGGCCTGCTTTAGAAAGTTCT  1350

Qy   1094  AGGAT  1098
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Db   1351  GCTGTGCTTCTGCCCTGCACCCGGAGATGCAGGTTTCTGATCGTGTGCGCAGCATTGCCA  1410
           AGGAT  1415
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RESULT 15
CNS04C2T/c

LOCUS   CNS04C2T   1053 bp   DNA   linear   GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
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            sequence.
ACCESSION   AL283934
VERSION   AL283934.1 GI:8022304
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1

Query Match   28.1%;   Score 324.2;   DB 9;   Length 879;
Best Local Similarity   63.4%;   Pred. No. 6.6e-74;
Matches 532;   Conservative   0;   Mismatches 298;   Indels   9;   Gaps   2;

AUTHORS　　Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
　　　　　　　Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
　　　　　　　Saurin,W. and Weissenbach,J.
TITLE　　　Estimate of human gene number provided by genome-wide analysis
　　　　　　　using Tetraodon nigroviridis DNA sequence
JOURNAL　　Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE　　20296633
PUBMED　　10835645
REFERENCE　2
AUTHORS　　Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
　　　　　　　Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
　　　　　　　Saurin,W., Bernot,A. and Weissenbach,J.
TITLE　　　Characterization and repeat analysis of the compact genome of the
　　　　　　　freshwater pufferfish Tetraodon nigroviridis
JOURNAL　　Genome Res. 10 (7), 939-949 (2000)
MEDLINE　　20359837
PUBMED　　10899143
REFERENCE　3　(bases 1 to 1053)
AUTHORS　　Genoscope.
TITLE　　　Direct Submission
JOURNAL　　Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
　　　　　　　BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
　　　　　　　- Web : www.genoscope.cns.fr)
COMMENT　　This sequence is a single read and was generated as part of a large
　　　　　　　scale clone-end sequencing project of the Tetraodon nigroviridis
　　　　　　　genome. For more information, please take a look at
　　　　　　　http://www.genoscope.cns.fr/Tetraodon.
FEATURES　　　　　　Location/Qualifiers
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　　　　　　　　　　/mol_type="genomic DNA"
　　　　　　　　　　/db_xref="taxon:99883"
　　　　　　　　　　/clone="098B06"
　　　　　　　　　　/clone_lib="G"
　　　　　　　　　　/note="Genoscope sequence ID : COBG098DA03SP1~end :
　　　　　　　　　　PUC-Ori"

ORIGIN

Query Match　　26.8%;　　Score 309.8;　　DB 9;　　Length 1053;
Best Local Similarity　65.3%;　　Pred. No. 4.2e-70;
Matches 587;　Conservative　8;　Mismatches 230;　Indels　74;　Gaps　7;

Qy　257 GATACACAAAGATGAAGACAGCAACCAACCATTACATATTTAACCTGCTTTGGCAGATG 316
Db　981 GGTACACCAAGATGAAGAGCACCGCCCACCAACATCATCATCCTTCAACYTGGCTYTYGGCCGACG 922

Qy　317 CTTTAGTTACTACAACCATGCCCTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTT 376
Db　921 CTYTAGCCACCAGCACCCTCCCCTTCCCAGAGCGCCAAGTACCTGAGTGMACACGTGGTCGT 862

Qy　377 TTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCACCAGCA 436
Db　861 TCGGGGAGCTGCTGTGCAAACTGGTCATCGTCATTGACTACTACAACATGTTCACCAGCA 802

Qy　437 TCTTCACCTTGA-CCATGATGAGCGTGGA-CCGCTACATTGCCGTGTGCCACCCCGT-GA 493
Db　801 TCTTCACCCTCACCCCATGATGAGCGTCGACCCGCTACGTTGCCKTTTGCCACCCCGGTCCC 742

Qy　494 AGGCTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGCATCTGCCTGC 553
Db　741 GGGGGAGCTGGACTTCCGCACACCCCCAGGCCCAAAATCATCAACGTGTTCATCTGGATCC 682

Qy　554 TGTCGTCATCGTTGGCGATCTCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGACG 613
Db　681 TCTCCTCAGCCGTCGGAGTGCCCGTGATGATGGCAGCGACGGAGACGGAGATAAAG 622

Qy　614 TCGA---------- 617
Db　621 GTGAGTGACGAGTCGGTGGCGTCGGCTCGCCAGCCAAGACTGTAACTTCGGTTCTTAC 562

Qy　618 ------TGTCATTGAGTGCTCCTTGCAGTTCCCAGATGATGACTACTCCTGGTGGAC 669
Db　561 CCGCCAGGGAACATCGCCGTGCATGCTCAGGTTCCCAAACCGGAGAGTACTGG---GAG 505

Qy　670 CTCTTCATGAAGATCTGGGTCTCATCTTTGCCTTCGTGATCCTGTCCTGTCATCATCATC 729
Db　504 ACGACCATGAAGTCTGCGTGTTCATCTTCGCCTTTGTGGTTCCGCCTCCTGGTCATCACC 445

Qy　730 GTCTGCTACACCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCGA 789
Db　444 ATCTGCTACGGGGCTGATGAT-CTGCGGCGTCAAGAGCGGTCCGGCTGCTCTCCGGGCTCCAAA 386

Qy　790 GAGAAAGATCGCAACCTGCGTAGGATCACCAGGACTGGTCCTGGTGGTGGCGAGTCTTC 849
Db　385 GAGAAGGACAGGAACCTCCGGGCGGATCACCGCCATGGTCCTGGTGGTGGGGCGCCTTC 326

Qy　850 GTCGTCTGCTGGACTCCCATTCACATATCATCCTGGTGGAGGCTCTCGGGGAGCACCTCC 909
Db　325 ATCGTCTGCTGGACTCCCATCCACATCTTCATCATGGTGTGTCCATCGAC 266

Qy　910 CAC---AGGACAGCTGCTCCTCTCCGCTATTACTTCTGGATCGCCTATACCAAC 966
Db　265 CACAAGAACCTGCTGGTGGTTGGCAGCTGGCACCTGGCATCCGCCTGGGCTACATGAAC 206

Qy・967 AGTAGCCTGAATCCCATTCCTACGCCTTTCTTGATGAAAATTCAAGGCGGGTGTTTCCG 1026
Db　205 AGCAGCCTGAACCGGGTCCTCTACGCCTTCCTGGACGAGAACTTCAAAAGGTGCTTCAGG 146

Qy　1027 GACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGGCAGAGCACTAGCAGAGTCCGAA 1085
Db　145 GACTTCTGCCTGCCCGCGCCGCGGTCCCGCCTGGAGMAGAACAGCTTCTCCAGAGCAGARAA 87

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